

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.  
OM protein - protein search, using sw model  
Run on: January 30, 2006, 08:52:05 ; Search time 45 Seconds  
(without alignments)  
288.446 Million cell updates/sec  
Title: US-09-716-356A-6  
Perfect score: 157  
Sequence: 1 YFGKLSKLSVIRNLDQVL.....LKKEDELGDRSIMFTVQNE 157  
Scoring table:  
Gapop 60.0 , Gapext 60.0  
Searched: 572060 seqs, 82675679 residues  
Word size : 0  
Total number of hits satisfying chosen parameters: 572060  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Listing first 100 summaries  
Database : Issued Parents AA:  
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2: /cgn2\_6/ptodata/1/iaa/6 COMB.pap:\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pap:\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pap:\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pap:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	156	99.4	157	1	US-08-896-605A-6
2	156	99.4	157	1	US-08-896-501A-4
3	156	99.4	157	2	US-08-884-324-1
4	156	99.4	157	2	US-08-996-338-26
5	156	99.4	157	2	US-08-558-818-1
6	156	99.4	157	2	US-08-974-469A-1
7	156	99.4	157	2	US-08-832-180-1
8	156	99.4	157	2	US-08-832-198-6
9	156	99.4	157	2	US-09-819-902-6
10	156	99.4	157	2	US-09-752-510-6
11	156	99.4	157	2	US-09-711-899-1
12	156	99.4	157	2	US-09-556-972-26
13	156	99.4	157	2	US-09-649-063-1
14	156	99.4	157	2	US-09-479-862-1
15	156	99.4	157	2	US-08-896-605A-2
16	156	99.4	157	2	US-08-896-501A-2
17	156	99.4	157	2	US-08-832-180-9
18	84	53.5	157	2	US-08-982-285-4
19	84	53.5	157	2	US-08-982-285-6
20	84	53.5	157	2	US-08-982-285-7
21	84	53.5	157	2	US-09-700-609-1
22	84	53.5	157	2	US-10-105-080-10
23	84	53.5	157	2	US-09-775-046-9
24	84	53.5	157	2	US-10-100-057-6
25	84	53.5	157	2	US-10-100-057-20
26	84	53.5	157	2	US-10-100-057-21
27	84	53.5	158	2	US-09-398-412B-7

28	84	53.5	164	2	US-09-949-016-10506	Sequence 10506, A
29	84	53.5	164	2	US-10-105-080-4	Sequence 4, Appli
30	84	53.5	164	2	US-09-949-016-6095	Sequence 6095, Ap
31	81	51.6	157	2	US-08-982-285-11	Sequence 11, Appl
32	81	51.6	157	2	US-10-100-057-25	Sequence 25, Appl
33	67	42.7	157	2	US-08-982-285-8	Sequence 8, Appli
34	67	42.7	157	2	US-10-100-057-22	Sequence 22, Appl
35	54	34.4	157	2	US-09-597-576-2	Sequence 2, Appli
36	53	33.8	157	2	US-08-982-285-9	Sequence 9, Appli
37	53	33.8	157	2	US-10-100-057-23	Sequence 23, Appl
38	50	31.8	50	2	US-08-832-198-2	Sequence 2, Appli
39	50	31.8	50	2	US-09-819-902-2	Sequence 2, Appli
40	50	31.8	50	2	US-09-752-510-2	Sequence 2, Appli
41	50	31.8	157	2	US-08-982-285-10	Sequence 10, Appl
42	50	31.8	157	2	US-08-982-285-12	Sequence 12, Appl
43	50	31.8	157	2	US-10-100-057-24	Sequence 24, Appl
44	50	31.8	157	2	US-10-100-057-26	Sequence 26, Appl
45	17	10.8	17	2	US-08-832-198-5	Sequence 5, Appli
46	17	10.8	17	2	US-09-819-902-5	Sequence 5, Appli
47	17	10.8	17	2	US-09-752-510-5	Sequence 5, Appli
48	17	10.8	17	2	US-10-100-057-13	Sequence 13, Appl
49	14	8.9	14	2	US-08-832-198-4	Sequence 4, Appli
50	14	8.9	14	2	US-09-819-902-4	Sequence 4, Appli
51	14	8.9	14	2	US-09-752-510-4	Sequence 4, Appli
52	14	8.9	14	2	US-10-100-057-12	Sequence 12, Appl
53	13	8.3	13	2	US-08-832-198-7	Sequence 7, Appli
54	13	8.3	13	2	US-09-819-902-7	Sequence 7, Appli
55	13	8.3	13	2	US-09-752-510-7	Sequence 7, Appli
56	13	8.3	13	2	US-10-100-057-11	Sequence 11, Appl
57	13	8.3	154	2	US-09-917-265A-5	Sequence 5, Appli
58	13	8.3	157	2	US-09-917-265A-12	Sequence 12, Appl
59	13	8.3	179	2	US-09-445-724B-14	Sequence 14, Appl
60	13	8.3	192	2	US-09-917-265A-8	Sequence 8, Appli
61	13	8.3	193	2	US-09-445-724B-2	Sequence 2, Appli
62	13	8.3	193	2	US-09-445-724B-6	Sequence 6, Appli
63	10	6.4	10	2	US-08-884-324-15	Sequence 15, Appl
64	10	6.4	10	2	US-08-832-180-7	Sequence 7, Appli
65	10	6.4	10	2	US-08-832-198-1	Sequence 1, Appli
66	10	6.4	10	2	US-08-832-198-3	Sequence 3, Appli
67	10	6.4	10	2	US-09-819-902-1	Sequence 1, Appli
68	10	6.4	10	2	US-09-819-902-3	Sequence 3, Appli
69	10	6.4	10	2	US-09-752-510-1	Sequence 1, Appli
70	10	6.4	10	2	US-09-752-510-3	Sequence 3, Appli
71	10	6.4	10	2	US-08-982-285-27	Sequence 27, Appl
72	10	6.4	10	2	US-09-479-862-15	Sequence 15, Appl
73	10	6.4	10	2	US-10-100-057-10	Sequence 10, Appl
74	10	6.4	10	2	US-10-100-057-15	Sequence 15, Appl
75	10	6.4	11	2	US-08-558-818-3	Sequence 3, Appli
76	10	6.4	11	2	US-08-974-469A-3	Sequence 3, Appli
77	10	6.4	11	2	US-09-711-899-3	Sequence 3, Appli
78	10	6.4	11	2	US-10-100-057-9	Sequence 9, Appli
79	10	6.4	133	2	US-09-917-265A-2	Sequence 2, Appli
80	7	4.5	7	2	US-10-100-057-3	Sequence 3, Appli
81	7	4.5	46	2	US-08-857-076-83	Sequence 83, Appl
82	7	4.5	46	2	US-09-205-658-83	Sequence 83, Appl
83	7	4.5	157	1	US-08-502-538A-2	Sequence 2, Appli
84	7	4.5	157	1	US-08-908-005A-2	Sequence 2, Appli
85	7	4.5	157	2	US-08-996-338-27	Sequence 27, Appl
86	7	4.5	157	2	US-08-558-818-7	Sequence 7, Appli
87	7	4.5	157	2	US-08-974-469A-7	Sequence 7, Appli
88	7	4.5	157	2	US-08-832-180-8	Sequence 8, Appli
89	7	4.5	157	2	US-08-832-198-11	Sequence 11, Appl
90	7	4.5	157	2	US-09-251-911-2	Sequence 2, Appli
91	7	4.5	157	2	US-09-251-911-2	Sequence 2, Appli
92	7	4.5	157	2	US-09-819-902-11	Sequence 11, Appl
93	7	4.5	157	2	US-09-752-510-11	Sequence 11, Appl
94	7	4.5	157	2	US-08-982-285-5	Sequence 5, Appli
95	7	4.5	157	2	US-08-982-285-13	Sequence 13, Appl
96	7	4.5	157	2	US-08-982-285-14	Sequence 14, Appl
97	7	4.5	157	2	US-09-711-899-7	Sequence 7, Appli
98	7	4.5	157	2	US-09-556-972-27	Sequence 27, Appl
99	7	4.5	157	2	US-09-700-609-2	Sequence 2, Appli
100	7	4.5	157	2	US-09-649-063-2	Sequence 2, Appli

## ALIGNMENTS

## RESULT 1

US-08-896-605A-6  
; Sequence 6, Application US/08896605A  
; Patent No. 5879942  
; GENERAL INFORMATION:  
; APPLICANT: TANIMOTO, Tadao  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 18 JULY 1997  
; APPLICATION NUMBER: US/08/896,605A  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 207,691/1996  
; FILING DATE: 19-JUL-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 156,062/1997  
; FILING DATE: 30-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: TANIMOTO=2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-896-605A-6

Query Match 99.4%; Score 156; DB 1; Length 157;  
Best Local Similarity 100.0%; Pred. No. 8.2e-157;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM	60
Db	1	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM	60
Qy	61	AVTISVCKEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQSVPGHDKNMQFESSY	120
Db	61	AVTISVCKEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQSVPGHDKNMQFESSY	120
Qy	121	EGYFLACEKRDLFKLIKKEDELGDRSIMFTVQNE	157
Db	121	EGYFLACEKRDLFKLIKKEDELGDRSIMFTVQNE	157

## RESULT 2

US-08-896-501A-4  
; Sequence 4, Application US/08896501A  
; Patent No. 5891663  
; GENERAL INFORMATION:  
; APPLICANT: TANIMOTO, Tadao  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 18 JULY 1997  
; APPLICATION NUMBER: US/08/896,605A  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 207,691/1996  
; FILING DATE: 19-JUL-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 156,062/1997  
; FILING DATE: 30-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: TANIMOTO=2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-896-501A-4

Query Match 99.4%; Score 156; DB 1; Length 157;  
Best Local Similarity 100.0%; Pred. No. 8.2e-157;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM	60
Db	1	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM	60
Qy	61	AVTISVCKEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQSVPGHDKNMQFESSY	120
Db	61	AVTISVCKEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQSVPGHDKNMQFESSY	120
Qy	121	EGYFLACEKRDLFKLIKKEDELGDRSIMFTVQNE	157
Db	121	EGYFLACEKRDLFKLIKKEDELGDRSIMFTVQNE	157

APPLICANT: TANIMOTO, Tadao  
APPLICANT: KURIMOTO, Masashi  
TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 18-JUL-1997  
APPLICATION NUMBER: US/08/896,501A  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 213,267/1996  
FILING DATE: 25-JUL-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 31,474/1997  
FILING DATE: 31-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: TANIMOTO=3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-896-501A-4

Query Match 99.4%; Score 156; DB 1; Length 157;  
Best Local Similarity 100.0%; Pred. No. 8.2e-157;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM	60
Db	1	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM	60
Qy	61	AVTISVCKEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQSVPGHDKNMQFESSY	120
Db	61	AVTISVCKEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQSVPGHDKNMQFESSY	120
Qy	121	EGYFLACEKRDLFKLIKKEDELGDRSIMFTVQNE	157
Db	121	EGYFLACEKRDLFKLIKKEDELGDRSIMFTVQNE	157

## RESULT 3

US-08-894-324-1  
; Sequence 1, Application US/08884324  
; Patent No. 6060283  
; GENERAL INFORMATION:  
; APPLICANT: Takanori OKURA  
; APPLICANT: Kakuji TORIGOE  
; APPLICANT: Masahi KURIMOTO  
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE  
; OF INDUCING THE PRODUCTION OF INTERFERON-  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington

APPLICANT: Takanori OKURA  
APPLICANT: Kakuji TORIGOE  
APPLICANT: Masahi KURIMOTO  
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE  
OF INDUCING THE PRODUCTION OF INTERFERON-  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington

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STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-884-324-1

Query Match          99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 8.2e-157;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNE 157

RESULT 4
US-08-996-338-26
Sequence 26, Application US/08996338
Patent No. 6087116
GENERAL INFORMATION:
APPLICANT: TORIGOE, Kakuji
APPLICANT: OKURA, Takanori
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
PRIOR APPLICATION DATA:

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-884-324-1

Query Match          99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 8.2e-157;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNE 157

RESULT 5
US-08-558-818-1
Sequence 1, Application US/08558818
Patent No. 6197297
GENERAL INFORMATION:
APPLICANT:
APPLICANT: NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO
APPLICANT: KUNIKATA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
WHICH INDUCES INTERFERON- PRODUCTION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELICI=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
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TELEFAX: (202) 737-3528
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,818
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA: JP 58,240/95
PRIOR APPLICATION DATA: February 23, 1995
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-558-818-1

Query Match          99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 8.2e-157;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVCKEKISXLSCKENKIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKKMQFESSY 120
Db 61 AVTISVCKEKISXLSCKENKIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
```

```
RESULT 6
US-08-974-469A-1
Sequence 1, Application US/08974469A
Patent No. 6207641
GENERAL INFORMATION:
APPLICANT: KENKYUJO
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: TORIGOE, Kakuiji
APPLICANT: TANIMOTO, Tadao
APPLICANT: FUKUDA, Shigeharu
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: AGENT FOR SUSCEPTIVE DISEASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,469A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/599,879
FILING DATE:
APPLICATION NUMBER: JP 78,357/95
FILING DATE: March 10, 1995
APPLICATION NUMBER: JP 274,988/95
FILING DATE: September 29, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE=1A
```

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-469A-1

Query Match          99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 8.2e-157;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVCKEKISXLSCKENKIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKKMQFESSY 120
Db 61 AVTISVCKEKISXLSCKENKIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 7
US-08-832-180-1
Sequence 1, Application US/08832180
Patent No. 6214584
GENERAL INFORMATION:
APPLICANT: KENKYUJO
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: USHIO, Shimpei
APPLICANT: TORIGOE, Kakuiji
APPLICANT: TANIMOTO, Tadao
APPLICANT: OKAMURA, Haruki
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,180
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/558,191
FILING DATE:
APPLICATION NUMBER: JP 304,203/94
FILING DATE: No. 6214584ember 15, 1994
APPLICATION NUMBER: 10048102
FILING DATE: September 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: USHIO=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
```



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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-832-180-1

Query Match          99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 8.2e-157;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQFORSVPGHNDKMQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQFORSVPGHNDKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 8
US-08-832-198-6
; Sequence 6, Application US/08832198
; Patent No. 6242255
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; APPLICANT: NUKADA, Yoshiyuki
; APPLICANT: FUJII, Mitsuakiyo
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; TITLE OF INVENTION: PRODUCTION BY IMMUNOCOMPETENT CELL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 08-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
; FILING DATE: 26-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-832-198-6

Query Match          99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 8.2e-157;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQFORSVPGHNDKMQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQFORSVPGHNDKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 9
US-09-819-902-6
; Sequence 6, Application US/09819902
; Patent No. 6403079
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; APPLICANT: NUKADA, Yoshiyuki
; APPLICANT: FUJII, Mitsuakiyo
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; TITLE OF INVENTION: PRODUCTION BY IMMUNOCOMPETENT CELL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 09/09/819,902
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/832,798
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
; FILING DATE: 26-SEP-1995
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
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TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" in position 73 is either
; 'Ile' or 'Thr'
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-819-902-6

Query Match          99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 8.2e-157;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFORSVPGHDNKMQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFORSVPGHDNKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 10
US-09-752-510-6
; Sequence 6, Application US/09752510
; Patent No. 6441138
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; NUKADA, Yoshiyuki
; FUJII, Mitsuaki
; TANIMOTO, Tadao
; KURIMOTO, Masaashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/752,510
; FILING DATE: 03-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528

TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" in position 73 is either
; 'Ile' or 'Thr'
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-752-510-6

Query Match          99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 8.2e-157;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFORSVPGHDNKMQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFORSVPGHDNKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 11
US-09-711-899-1
; Sequence 1, Application US/09711899
; Patent No. 6509449
; GENERAL INFORMATION:
; APPLICANT: <Unknown>
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,899
; FILING DATE: 13-No. 6509449-2000
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/588,818
; FILING DATE: 2000-11-15
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: FELICI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-711-899-1
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Query Match 99.4%; Score 156; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 8.2e-157;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNPRTIFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNPRTIFIISMVKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHNDKMQFESSY 120  
DB 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHNDKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 12  
US-09-556-972-26  
; Sequence 26, Application US/09556972  
; Patent No. 6559298  
; GENERAL INFORMATION:  
; APPLICANT: TORIGOE, Kakuji  
; OKURA, Takanori  
; KURIMOTO, Musashi  
; TITLE OF INVENTION: POLYPEPTIDES  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/556,972  
; FILING DATE: 24-Apr-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/996,338  
; FILING DATE: 22-DEC-1997  
; APPLICATION NUMBER: JP 74,697/1997  
; FILING DATE: 12-MAR-1997  
; APPLICATION NUMBER: JP 215,488/1997  
; FILING DATE: 28-JUL-1997  
; APPLICATION NUMBER: JP 291,837/1997  
; FILING DATE: 09-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: TORIGOE=3  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-09-556-972-26

Query Match 99.4%; Score 156; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 8.2e-157;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNPRTIFIISMVKDSQPRGM 60

DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNPRTIFIISMVKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHNDKMQFESSY 120  
DB 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHNDKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 13  
US-09-649-063-1  
; Sequence 1, Application US/09649063  
; Patent No. 6600022  
; GENERAL INFORMATION:  
; APPLICANT: TORIGOE, Kakuji  
; USHIO, Shimpel  
; KUNIKATA, Toshio  
; KURIMOTO, Masashi  
; TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/649,063  
; FILING DATE: 29-Aug-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/996,140  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: JP 52,526/1997  
; FILING DATE: 21-FEB-1997  
; APPLICATION NUMBER: JP 163,490/1997  
; FILING DATE: 6-JUN-1997  
; APPLICATION NUMBER: JP 215,490/1997  
; FILING DATE: 28-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: TORIGOE=2  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-649-063-1

Query Match 99.4%; Score 156; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 8.2e-157;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNPRTIFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNPRTIFIISMVKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHNDKMQFESSY 120

Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFFORSVPGHDNKKQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
RESULT 14  
US-09-479-862-1  
; Sequence 1, Application US/09479862  
; Patent No. 6790442  
; GENERAL INFORMATION:  
; APPLICANT: Takatori OKURA  
; APPLICANT: Kakuji TORIOGE  
; APPLICANT: Masahi KURIMOTO  
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE  
; TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/479,862  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/894,324  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: OKURA=1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-479-862-1  
Query Match 99.4%; Score 156; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 8.2e-157;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFFORSVPGHDNKKQFESSY 120  
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFFORSVPGHDNKKQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
RESULT 15  
US-08-896-605A-2  
; Sequence 2, Application US/08896605A  
; Patent No. 5879942

; GENERAL INFORMATION:  
; APPLICANT: TANIMOTO, Tadao  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/896,605A  
; FILING DATE: 18 July 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 207,691/1996  
; FILING DATE: 19-JUL-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 156,062/1997  
; FILING DATE: 30-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: TANIMOTO=2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 193 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-896-605A-2  
Query Match 99.4%; Score 156; DB 1; Length 193;  
Best Local Similarity 100.0%; Pred. No. 1e-156;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60  
Db 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 96  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFFORSVPGHDNKKQFESSY 120  
Db 97 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFFORSVPGHDNKKQFESSY 156  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193  
RESULT 16  
US-08-896-501A-2  
; Sequence 2, Application US/08896501A  
; Patent No. 5891663  
; GENERAL INFORMATION:  
; APPLICANT: TANIMOTO, Tadao  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.

COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/896,501A  
FILING DATE: 18-JUL-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 213,267/1996  
FILING DATE: 25-JUL-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 31,474/1997  
FILING DATE: 31-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: TANIMOTO-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 193 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-896-501A-2

Query Match 99.4%; Score 156; DB 1; Length 193;  
Best Local Similarity 100.0%; Pred. No. le-156;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFITISMYKDSQPRGM 60  
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFITISMYKDSQPRGM 96  
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQSVPGHNDKMQFESSY 120  
DB 97 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQSVPGHNDKMQFESSY 156  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 17  
US-08-832-180-9  
Sequence 9, Application US/08832180  
Patent No. 6214584  
GENERAL INFORMATION:  
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU  
APPLICANT: KENYUJO  
APPLICANT: USHIO, Shimei  
APPLICANT: TORIGOE, Kakuji  
APPLICANT: TANIMOTO, Tadao  
APPLICANT: OKAMURA, Haruki  
APPLICANT: KURIMOTO, Masashi  
TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street N.W. Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect Version 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/832,180  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/558,191  
FILING DATE:  
APPLICATION NUMBER: JP 304,203/94  
FILING DATE: No. 6214584ember 15, 1994  
APPLICATION NUMBER: 10048102  
FILING DATE: September 18, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Browdy, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: USHIO=1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 193 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-832-180-9

Query Match 99.4%; Score 156; DB 2; Length 193;  
Best Local Similarity 100.0%; Pred. No. le-156;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFITISMYKDSQPRGM 60  
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFITISMYKDSQPRGM 96  
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQSVPGHNDKMQFESSY 120  
DB 97 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQSVPGHNDKMQFESSY 156  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 18  
US-08-982-285-4  
Sequence 4, Application US/08982285  
Patent No. 6476197  
GENERAL INFORMATION:  
APPLICANT: YAMAMOTO, Koza  
APPLICANT: OKAMOTO, Iwao  
APPLICANT: KURIMOTO, Masashi  
TITLE OF INVENTION: POLYPEPTIDES  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
STREET: 419 7th Street N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/982,285  
FILING DATE:  
PRIOR APPLICATION DATA:

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/ APPLICATION NUMBER: JP 333,037/96
/ FILING DATE: No. 6476197ember 29, 1996
/ APPLICATION NUMBER: JP 20,906/97
/ FILING DATE: January 21, 1997
/ APPLICATION NUMBER: JP 10,053,503
/ FILING DATE: No. 6476197ember 14, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BROWDY, Roger L.
/ REGISTRATION NUMBER: 25,618
/ REFERENCE/DOCKET NUMBER: YAMAMOTO=15
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 157 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-982-285-4
/
Query Match 53.5%; Score 84; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 9e-81;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 74 LSCENKIISFKEMNPPDNIKDKTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133
DB 74 LSCENKIISFKEMNPPDNIKDKTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133
OY 134 FKLILKKEDELGRSIMFTVQNEED 157
DB 134 FKLILKKEDELGRSIMFTVQNEED 157

RESULT 19
US-08-982-285-6
/ Sequence 6, Application US/08982285
/ Patent No. 6476197
/ GENERAL INFORMATION:
/ APPLICANT: YAMAMOTO, Kozo
/ APPLICANT: OKAMOTO, Iwao
/ APPLICANT: KURIMOTO, Masashi
/ TITLE OF INVENTION: POLYPEPTIDES
/ NUMBER OF SEQUENCES: 51
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
/ STREET: 419 7th Street N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 333,037/96
/ FILING DATE: No. 6476197ember 29, 1996
/ APPLICATION NUMBER: JP 20,906/97
/ FILING DATE: January 21, 1997
/ APPLICATION NUMBER: JP 10,053,503
/ FILING DATE: No. 6476197ember 14, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BROWDY, Roger L.
/ REGISTRATION NUMBER: 25,618
/ REFERENCE/DOCKET NUMBER: YAMAMOTO=15
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 157 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-982-285-7
/
Query Match 53.5%; Score 84; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 9e-81;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 74 LSCENKIISFKEMNPPDNIKDKTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133
DB 74 LSCENKIISFKEMNPPDNIKDKTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133
OY 134 FKLILKKEDELGRSIMFTVQNEED 157
DB 134 FKLILKKEDELGRSIMFTVQNEED 157

RESULT 20
US-08-982-285-7
/ Sequence 7, Application US/08982285
/ Patent No. 6476197
/ GENERAL INFORMATION:
/ APPLICANT: YAMAMOTO, Kozo
/ APPLICANT: OKAMOTO, Iwao
/ APPLICANT: KURIMOTO, Masashi
/ TITLE OF INVENTION: POLYPEPTIDES
/ NUMBER OF SEQUENCES: 51
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
/ STREET: 419 7th Street N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 333,037/96
/ FILING DATE: No. 6476197ember 29, 1996
/ APPLICATION NUMBER: JP 20,906/97
/ FILING DATE: January 21, 1997
/ APPLICATION NUMBER: JP 10,053,503
/ FILING DATE: No. 6476197ember 14, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BROWDY, Roger L.
/ REGISTRATION NUMBER: 25,618
/ REFERENCE/DOCKET NUMBER: YAMAMOTO=15
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 157 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-982-285-7
/
Query Match 53.5%; Score 84; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 9e-81;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 74 LSCENKIISFKEMNPPDNIKDKTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133
DB 74 LSCENKIISFKEMNPPDNIKDKTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133
OY 134 FKLILKKEDELGRSIMFTVQNEED 157
DB 134 FKLILKKEDELGRSIMFTVQNEED 157
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Db 74 LSCENKIISFKEMPPDNKDKTSIIFFQRSVPGHDKMKQFESSSYEGYFLACEKRD 133  
QY 134 FKILKKEDELGDRSIMFTVQNE 157  
Db 134 FKILKKEDELGDRSIMFTVQNE 157

RESULT 21  
US-09-700-609-1  
; Sequence 1, Application US/09700609  
; Patent No. 6582689  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Randall K  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: P50777  
; CURRENT APPLICATION NUMBER: US/09/700,609  
; CURRENT FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/086,560  
; PRIOR FILING DATE: 1999-05-21  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Human  
US-09-700-609-1

Query Match 53.5%; Score 84; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 9e-81;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 74 LSCENKIISFKEMPPDNKDKTSIIFFQRSVPGHDKMKQFESSSYEGYFLACEKRD 133  
Db 74 LSCENKIISFKEMPPDNKDKTSIIFFQRSVPGHDKMKQFESSSYEGYFLACEKRD 133  
QY 134 FKILKKEDELGDRSIMFTVQNE 157  
Db 134 FKILKKEDELGDRSIMFTVQNE 157

RESULT 22  
US-10-105-080-10  
; Sequence 10, Application US/10105080  
; Patent No. 6800479  
; GENERAL INFORMATION:  
; APPLICANT: SAMYANG GENEX CORPORATION  
; TITLE OF INVENTION: RECOMBINANT ADENOVIRUSES EXPRESSING INTERLEUKIN-18 PROTEIN AND  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/105,080  
; CURRENT FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: KR 10-2001-78296  
; PRIOR FILING DATE: 2001-12-11  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Kopatentin 1.71  
; SEQ ID NO 10  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Human mature interleukin-18 mutant  
US-10-105-080-10

Query Match 53.5%; Score 84; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 9e-81;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 74 LSCENKIISFKEMPPDNKDKTSIIFFQRSVPGHDKMKQFESSSYEGYFLACEKRD 133  
Db 74 LSCENKIISFKEMPPDNKDKTSIIFFQRSVPGHDKMKQFESSSYEGYFLACEKRD 133  
QY 134 FKILKKEDELGDRSIMFTVQNE 157  
Db 134 FKILKKEDELGDRSIMFTVQNE 157

RESULT 23  
US-09-775-046-9  
; Sequence 9, Application US/09775046  
; Patent No. 6843987  
; GENERAL INFORMATION:  
; APPLICANT: Debets, Johannes Eduard Maria Antonius  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Bazan, J. Fernando  
; APPLICANT: Kastelein, Robert A.  
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS  
; FILE REFERENCE: DX01073K  
; CURRENT APPLICATION NUMBER: US/09/775,046  
; CURRENT FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 60/179,638  
; PRIOR FILING DATE: 2000-02-02  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-775-046-9

Query Match 53.5%; Score 84; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 9e-81;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 74 LSCENKIISFKEMPPDNKDKTSIIFFQRSVPGHDKMKQFESSSYEGYFLACEKRD 133  
Db 74 LSCENKIISFKEMPPDNKDKTSIIFFQRSVPGHDKMKQFESSSYEGYFLACEKRD 133  
QY 134 FKILKKEDELGDRSIMFTVQNE 157  
Db 134 FKILKKEDELGDRSIMFTVQNE 157

RESULT 24  
US-10-100-057-6  
; Sequence 6, Application US/10100057  
; Patent No. 6896880  
; GENERAL INFORMATION:  
; APPLICANT: GILLISPIE, Matthew Todd  
; HORWOOD, Nicole Joy  
; UDAGAWA, No. 6896880yuyuki  
; KURIMOTO, Masashi  
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/100,057  
; FILING DATE: 19-Mar-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,061  
; FILING DATE: 25-FEB-1998  
; APPLICATION NUMBER: JP 55,468/1997  
; FILING DATE: 25-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: GILLISPIE=1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-100-057-6

Query Match 53.5%; Score 84; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 9e-81; Mismatches 0; Indels 0; Gaps 0;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 74 LSCENKIISFKEMNPPDNIKDKSDIIFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133  
DB 74 LSCENKIISFKEMNPPDNIKDKSDIIFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133  
QY 134 FKLILKKEDELGDRSIMFTVQNEED 157  
DB 134 FKLILKKEDELGDRSIMFTVQNEED 157

RESULT 25  
US-10-100-057-20  
; Sequence 20, Application US/10100057  
; Patent No. 6896880  
GENERAL INFORMATION:  
APPLICANT: GILLISPIE, Matthew Todd  
HORWOOD, Nicole Joy  
UDAGAWA, No. 6896880uyuki  
KURIMOTO, Masashi  
TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/10/100,057  
FILING DATE: 19-Mar-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/030,061  
FILING DATE: 25-FEB-1998  
APPLICATION NUMBER: JP 55,468/1997  
FILING DATE: 25-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: GILLISPIE=1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-10-100-057-20

Query Match 53.5%; Score 84; DB 2; Length 157;

Best Local Similarity 100.0%; Pred. No. 9e-81; Mismatches 0; Indels 0; Gaps 0;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 74 LSCENKIISFKEMNPPDNIKDKSDIIFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133  
DB 74 LSCENKIISFKEMNPPDNIKDKSDIIFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133  
QY 134 FKLILKKEDELGDRSIMFTVQNEED 157  
DB 134 FKLILKKEDELGDRSIMFTVQNEED 157

Search completed: January 30, 2006, 08:59:52.  
Job time : 45 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2006, 08:30:42 ; Search time 39 Seconds  
(without alignments)  
387.334 Million cell updates/sec

Title: US-09-716-356A-6  
Perfect score: 812  
Sequence: 1 YFGKLESKLSVIRNLDQVL.....LKKDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 80:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	515	63.4	192	2 S60226	cytokine IGIF - mo
2	85	10.5	381	2 T40341	hypothetical prote
3	82	10.1	263	2 T39487	hypothetical prote
4	81.5	10.0	270	1 S10532	interleukin-1 alph
5	80.5	9.9	866	2 C71509	probable DNA polym
6	79	9.7	452	2 D64583	hypothetical prote
7	78.5	9.7	204	2 T43357	hypothetical prote
8	78	9.6	473	2 T32038	hypothetical prote
9	77.5	9.5	1251	2 A56677	neural cell cycl
10	77	9.5	364	2 A81261	probable periplasm
11	76	9.4	632	2 T00679	hypothetical prote
12	76	9.4	747	2 E84698	hypothetical prote
13	75.5	9.3	192	2 S15620	(2'-5')oligo(A) sy
14	75.5	9.3	270	2 I46620	interleukin-1 alph
15	75.5	9.3	1036	2 H64245	hypothetical prote
16	75.5	9.3	1663	1 C3MS	complement C3 prec
17	75	9.2	1064	1 S57450	protein-tyrosine k
18	75	9.2	2470	2 I50726	cation-independent
19	74.5	9.2	334	2 T04198	hypothetical prote
20	74.5	9.2	389	2 B69277	TRK potassium upa
21	74.5	9.2	467	2 A48713	serine/threonine-s
22	74.5	9.2	1228	2 A57384	multimerin, endoth
23	74.5	9.2	1510	2 T16927	hypothetical prote
24	74	9.1	245	2 B30488	hypothetical prote
25	74	9.1	361	2 E36904	mand family ATPase
26	74	9.1	376	2 T24925	hypothetical prote
27	74	9.1	467	2 I49609	proto-oncogene pro
28	74	9.1	467	2 A47388	serine/threonine p
29	74	9.1	680	2 A28121	major merozoite su

30	74	9.1	810	2 B71639	virb4 protein prec
31	74	9.1	1772	2 A45532	major merozoite su
32	73.5	9.1	268	2 H85641	probable small sub
33	73.5	9.1	268	2 C90781	probable small sub
34	73	9.0	418	2 D82932	seryl-tRNA synthet
35	73	9.0	447	2 T26293	hypothetical prote
36	72.5	8.9	268	1 B24073	interleukin-1 alph
37	72.5	8.9	313	2 C96528	protein F27J15.10
38	72.5	8.9	436	2 G97701	polynucleotide ade
39	72.5	8.9	475	2 T32036	hypothetical prote
40	72.5	8.9	888	2 A38539	pl01 protein precu
41	72.5	8.9	1246	2 S60954	probable membrane
42	72.5	8.9	1294	2 T48349	ElN2 protein - Ara
43	72.5	8.9	1997	2 F71607	DNA helicase II BR
44	72	8.9	264	2 B90051	hypothetical prote
45	72	8.9	1613	2 S39059	protein BRG1 - hum
46	71.5	8.8	268	1 ICBOJA	interleukin-1 alph
47	71.5	8.8	425	2 T25457	hypothetical prote
48	71.5	8.8	485	2 A11636	weakly probable su
49	71.5	8.8	586	2 C70091	conserved hypotet
50	71.5	8.8	845	2 T46164	nodulin / glutamat
51	71	8.7	318	2 H96917	ABC transporter, A
52	71	8.7	343	2 G71979	probable type II D
53	71	8.7	382	2 H90127	Mrs2p [imported] -
54	71	8.7	450	2 G71928	hypothetical prote
55	71	8.7	581	2 S46327	gene cel IF A3 pro
56	71	8.7	698	2 JH0163	No-on-transient A
57	71	8.7	700	2 JH0162	No-on-transient A
58	71	8.7	1367	2 T18466	hypothetical prote
59	71	8.7	2441	2 D71623	erythrocyte membra
60	70.5	8.7	260	2 F89809	hypothetical prote
61	70.5	8.7	268	1 A61246	interleukin-1 alph
62	70.5	8.7	578	2 H82872	hypothetical prote
63	70.5	8.7	644	2 S64135	hypothetical prote
64	70.5	8.7	753	2 T19338	hypothetical prote
65	70.5	8.7	1278	2 B70236	hypothetical prote
66	70	8.6	198	1 MNXRA	minor outer capsid
67	70	8.6	205	2 E96653	hypothetical prote
68	70	8.6	354	2 E97128	magnesium and coba
69	70	8.6	381	2 H96656	hypothetical prote
70	70	8.6	393	2 D97275	glycosyltransferas
71	70	8.6	658	2 T32893	hypothetical prote
72	70	8.6	1064	2 S74861	hypothetical prote
73	70	8.6	1647	2 S45252	SNF2beta protein -
74	70	8.6	1738	2 T14867	interactin - slime
75	70	8.6	2663	1 S28261	centromere translati
76	69.5	8.6	351	2 E71372	probable translati
77	69.5	8.6	375	2 T29568	hypothetical prote
78	69.5	8.6	447	2 B97338	biotin carboxylase
79	69.5	8.6	582	2 S29314	phytoene dehydroge
80	69.5	8.6	728	2 T24716	hypothetical prote
81	69.5	8.6	871	2 T48502	hypothetical prote
82	69.5	8.6	919	1 RN2VCA	DNA-directed RNA p
83	69.5	8.6	967	2 D72308	conserved hypotet
84	69	8.5	273	2 T51512	hypothetical prote
85	69	8.5	516	2 S14694	hypothetical prote
86	69	8.5	572	2 F90297	ATP-dependent RNA
87	69	8.5	1071	2 T04926	starch synthase ho
88	68.5	8.4	263	2 A97498	hypothetical prote
89	68.5	8.4	270	1 ICMS1	interleukin-1 alph
90	68.5	8.4	287	2 D69536	hypothetical prote
91	68.5	8.4	287	2 A92716	conserved hypotet
92	68.5	8.4	331	2 A26467	isopenicillin N sy
93	68.5	8.4	331	2 S04441	isopenicillin N sy
94	68.5	8.4	432	2 G90268	conserved hypotet
95	68.5	8.4	476	2 A97180	fes oxidoreductase
96	68.5	8.4	521	2 B71717	hypothetical prote
97	68.5	8.4	535	2 B49804	Hsp90 homolog p61
98	68.5	8.4	706	2 S38168	hypothetical prote
99	68	8.4	232	2 B90558	hypothetical prote
100	68	8.4	351	2 B97273	uncharacterized pr

RESULT 3

T39487

hypothetical protein SPBC15D4.11c - fission yeast (*Schizosaccharomyces pombe*)

C:Species: *Schizosaccharomyces pombe*

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C:Accession: T39487

R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lucas, M.; Gaillardin, C.

submitted to the EMBL Data Library, August 1997

A:Reference number: Z21858

A:Accession: T39487

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-263 <LYN>

A:Cross-references: UNIPROT:O74315; UNIPARC:UPI000006ABF8; EMBL:AL031349; PIDN:CAA20486

A:Experimental source: strain 972H-; cosmid c1504

C:Genetics:

A:Gene: SPDB:SPBC15D4.11c

A:Map position: 2

A:Introns: 96/2; 147/3

C:Superfamily: *Schizosaccharomyces pombe* hypothetical protein SPBC15D4.11c

Query Match 10.1%; Score 82; DB 2; Length 263;  
Best Local Similarity 21.7%; Pred.No. 2.3;  
Matches 35; Conservative 33; Mismatches 65; Indels 28; Gaps 5;

Qy 4 KLEKLSVIRNLNDQVLFDIQGNRPFLFEDMTDSDCRDNAPRTTIFIISMYKDSQPRGMAVT 63  
|||:::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
Db 47 KLDSELGVYKVQLDETLPKKGYEKALHSFIHED-----PSLNYISALKETAKERTVT 100  
|||:::||::||::||::||::||::||::||::||::||::||::||::||::||  
Qy 64 ISVKCFKIXSLSCENKIIGFKENVPPDNTIKDTKSDIIFQRSVPGH----- 109  
::||::||::||::||::||::||::||::||::||::||::||::||::||  
Db 101 VPVYSRKSV--QTKPITHSAEN--ENGNETSDELVFVFOHSIPAYVQLTNHGHTILCAL 156  
::||::||::||::||::||::||::||::||::||::||::||::||::||  
Qy 110 ---DNKKQFESSYEGYFLACEKERDLFKLIILKKEDELGDR 147  
::||::||::||::||::||::||::||::||::||::||::||::||::||  
Db 157 ILCKGMLHPDISIFSGFSPONSOAFSSDL-RLIILOKSOKYTR 196  
::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 4  
S10532  
interleukin-1 alpha precursor - pig  
N;Alternate names: hematopoietin-1; IL-1 alpha  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 20-Feb-1995 #sequence\_revision 22-Nov-1996 #text\_change 09-Jul-2004  
C;Accession: S10532  
R;Maliszewski, C.R.; Renshaw, B.R.; Schoenborn, M.A.; Urban, J.F.; Baker, P.E.  
Nucleic Acids Res. 18, 4282, 1990  
A;Title: Porcine IL-1 alpha cDNA nucleotide sequence.  
A;Reference number: S10532; MUID:90332454; PMID:2377484  
A;Accession: S10532  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-270 <MAL>  
A;Cross-references: UNIPROT:PI8430; UNIPARC:UPI0000012D493; EMBL:X52731; NID:G1987; PIDN  
C;Comment: Produced by activated macrophages, the IL-1 proteins stimulate thymocyte pro  
C;Comment: IL-1 proteins are involved in the inflammatory response, being identified as

[illegible]

Db	123	KYFMRVINHQCILNDARNQSIIRPDSGOYLMAAVLNLDDEAVKFDMAAYTENDOSQLPV	182
Qy	63	TISVCKEIKSLXSCEN--KILSEKEM-NPPDNIKOTKSDIIIFQSRVPGHDNNKMOFESS	119
Db	183	TLRIS-ETRLFVSQNEDEPVLKELPPTKTIKQETSLLFWEK----HGNMDFKSA	237
Qy	120	YEGYFLACEKER	131
Db	238	HPKLEIATRQEK	249

RESULT 5  
C71509  
probable DNA polymerase I,- Chlamydia trachomatis (serotype D, strain UW3/Cx)  
C:Species: Chlamydia trachomatis  
C:Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004  
C:Accession: C71509  
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998  
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis  
A:Reference number: A71570; MUID:99000809; PMID:9784136  
A:Accession: C71509  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-866 <ARN>  
A:Cross-references: UNIPROT:O84500; UNIPARC:UPT000000D3352; GB:AE001273; NID  
A:Experimental source: serotype D, strain UW-3/Cx  
C:Genetics:  
C:Gene: polA  
C:Superfamily: DNA-directed DNA polymerase I

RESULT 6  
D64583  
hypothetical protein HP0508 - Helicobacter pylori (strain 26695)  
C:Species: Helicobacter pylori  
C:Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004  
C:Accession: D64583  
R:Tombl, J.F.; White, O.; Kervlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997  
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Praeger, C. A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A:Reference number: A64520, MUID:97394467; PMID:9252185  
A:Accession: D64583  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-452 <TOM>

Db 105 LVYFQFNQA-FLIAPNDELYEQIRATNTDINFSSDLLVTFNLGFDPKIANLRKACNV 163

QY 59 -GMAVTISVCKEKISXUSCEN-KIISFKEMPPNDIKDSDIIIFQRSVPGHD----NK 112

Db 164 YSGVGIYIVTNTNLISCEFEILEKREL---DTSGVTKTSTPPFSR-VEGIDAGTLGK 219

QY 113 MQPSSSVGEYF---LACEERDLFKLILKKEDELDGRSIMFTVONE 156

Db 220 L-FSGSOSKNYFAYYDAIVLKKEKEVYIKVPEEKIDSFETKKTQF 266

RESULT 7  
T44357  
hypothetical protein [imported] - Clostridium histolyticum  
C/Species: Clostridium histolyticum  
C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C/Accession: T44357  
R./Matsumita, O.; Jung, C.M.; Katayama, S.; Minami, J.; Takahashi, Y.; Okabe, A.  
J. Bacteriol. 181, 923-933, 1999  
A./Title: Gene duplication and multiplicity of collagenases in Clostridium histolyticum  
A./Reference number: 222752; MUID:99121032; PMID:9922257  
A./Accession: T44357  
A./Status: preliminary; translated from GB/EMBL/DBJ  
A./Molecule type: DNA  
A./Residues: 1-204 <MAT>  
A./Cross-references: UNIPROT:Q92NU7; UNIPARC:UPI00000B182D; EMBL:AB014075; NID:g3868863  
A./Experimental source: strain JCM 1403

RESULT 8  
T32038  
hypothetical protein F41B5.2 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T32038  
R:Dante, M.; Kramer, J.  
submitted to the EMBL Data Library, July 1997  
A;Description: The sequence of *C. elegans* cosmid F41B5.  
A;Reference number: Z21115  
A;Accession: T32038  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-473 <DNA>  
A;Cross-references: UNIPROT:O16673; UNIPARC:UPI0000080265; EMBL:AF016676; PIDN:AAC2590.  
A;Experimental source: strain Bristol N2; clone F41B5

```
QY 10 SVIRNLNDQVLF---IDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGMATISV 66
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 NALANVINQITFGYRFDESNOEYKXKH-----LIEFOENVFTSAKVTVOV 216
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 KCEKIXLSCENKIIISFKNPNPDNIKOTKSDII-PQRSVPGHDKMKQFESSSYEGYFL 125
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 217 FAPKL-----GKILPGESLE--DLMKWKNYSYDFNTQIENHROKIDFDSSESQDYAE 268
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 126 ACKERDLFKLILKXGDELGDRSIMFTVQ 154
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 269 AYLKEQ-----KKYEALGDTLFSNKQ 290
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
A56677
neural cell cycle withdrawal protein ON1 - quail (fragment)
C:Species: Coturnix coturnix (quail)
C>Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
C:Accession: A56677
R:Bidou, L.; Crisanti, P.; Blancher, C.; Pessac, B.
Mech. Dev. 43, 159-173, 1993
A:Title: A novel cDNA corresponding to transcripts expressed in retina post-mitotic neu
A:Reference number: A56677; MUID:94128599; PMID:8297788
A:Accession: A56677
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1251 <BID>
A:Cross-references: UNIPROT:Q91365; UNIPARC:UPI00000FB847; GB:S68151; NID:G545153; PIDN:
A>Note: conceptual translation not given

Query Match 9.5%; Score 77.5; DB 2; Length 1251;
Best Local Similarity 23.5%; Pred. No. 38;
Matches 38; Conservative 37; Mismatches 64; Indels 23; Gaps 9;

QY 6 ESKLSVI-RNLNDQVLF---DQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGMA 61
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 648 EEKLAQIQEMDEQVIOGYQENELRYKQMKDLQIQNKNEE-----QMYKENQCL-MS 702
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 62 VITSVKCEKISLSCENKIIISFKEMPPDNIKDTSIIFFQRSVPGHDKMKQF----- 116
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 703 ELIALR-EKVERINIOSIV--RESEPARN--QSFTELISELGAARKEETKLEERIRLK 757
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 117 --SSSYEGVFLACEKRDLPKILKXGDELGDRSIMFTVQNE 156
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 758 QDKQALELDLQAKERDLAKVQITSTS--SEKSYBFKIMEE 797
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
A81261
probable periplasmic protein Cjl643 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: A81261
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: A81261
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <PAR>
A:Cross-references: UNIPROT:Q9PM33; UNIPARC:UPI00000C1FAB; GB:AL1139079; GB:AL111169; NID
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cjl643

Query Match 9.5%; Score 77; DB 2; Length 364;
Best Local Similarity 24.8%; Pred. No. 9;
Matches 38; Conservative 21; Mismatches 40; Indels 54; Gaps 9;

QY 12 IRNLNDQVLFIDQGNRPLFEDMTDSDCRD-NAPRTFIISMYK-----DSQPR----- 58
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
Db 211 LRLKNEKILFARGSTLYFQVLRDN--MDLNISTEVFAKUSKFNLPDSKPKPKITNFTS 268
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 59 --GMAVTISVKCEKI-----SXLSCENKII-SFKEMNPPDNI----- 92
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 269 NLGLTVNASLVVTKIDPKSKVSNAGFMVGDKILRVNNILANNFKEL---QNILSAGNDFS 325
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 93 -----KOTKSDIIFFQRSVPGH-----DNKMQF 115
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 326 ILIERKSTKLPLSNFNNELGGNANSGGDGKQFQ 358
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
T00679
hypothetical protein At2g43990 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F6E13.12
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00679; A84873
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, June 1998
A:Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.
A:Reference number: Z14180
A:Accession: T00679
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-632 <ROU>
A:Cross-references: UNIPROT:O80569; UNIPARC:UPI00000A05B0; EMBL:AC004005; NID:G3212846;
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84873
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-632 <STO>
A:Cross-references: UNIPARC:UPI00000A05B0; GB:AE002093; NID:G3212856; PIDN:AAC23407.1;
C:Genetics:
A:Gene: At2g43990; F6E13.12
A:Map position: 2

Query Match 9.4%; Score 76; DB 2; Length 632;
Best Local Similarity 25.6%; Pred. No. 24;
Matches 34; Conservative 29; Mismatches 40; Indels 30; Gaps 9;

QY 28 PLFEDMTDSD-CRDNAPRTFIISMYKDSQPRGMATISVKCEK-----ISXLSCENK 79
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 368 PLSDRSASSDLQNTSSGRLSPMDIYKETTR---ISSLSNPLFRFRFHLSSCDGE 424
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 80 IISFK-----EMNPPDNIKDTSIIFFQRSVP--GHDNMQF--ESSSYEGYF-LACBK 129
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 425 ASAPDTSPTCELDPEHLKGDKSSPL----SVDTLGSENVIQTPESNSFDNYFGLSCSQ 480
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 130 ERDLFKLILKXED 142
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 481 AE-----IQKXHD 488
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
E84698
hypothetical protein At2g29620 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: E84698
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
```



```

Qy 71 -ISXLSCKNLIISFKEMNPPDNIKDTKSDIIFORSVPGHDNKMOPSSSYEGYFLACEK 129
Db 905 FIKGVNDNQVFSISY-----DLKITNNQTLIV-DANGFDNSIWFDTIS-----EN 950
Qy 130 ERDLFKLI---LKKEDLGDRSIMEYVONED 157
Db 951 QTQLFKALSFYLKONNLQFKRVPDFNLKSQD 981

```

Search completed: January 30, 2006, 08:41:03  
 Job time : 43 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2006, 08:29:42 ; Search time 161 Seconds

(without alignments)  
688,000 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLESKLVRLNDQVL.....LKKEDELGDRSMTFTQVED 157

Scoring table: BLOSUM62 , Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	811	99.9	189	2	Q6WJ7 HUMAN
2	811	99.9	193	1	IL18 HUMAN
3	811	99.9	193	2	Q6FGY3 HUMAN
4	798	98.3	193	2	Q96KJ8 HUMAN
5	792	97.5	193	2	Q9BG15 MACMU
6	659	81.2	193	1	IL18 HORSE
7	659	81.2	193	2	Q6TLW4 BUBBU
8	659	81.2	193	2	Q6T573 BUBBU
9	654	80.5	178	2	Q9WZL8 BOVIN
10	654	80.5	193	1	IL18 BOVIN
11	651	80.2	193	2	Q51931 BOSTR
12	648	79.8	193	2	Q9GL09 SHEEP
13	647	79.7	159	2	Q6QVCA CAPI
14	637	78.4	192	1	IL18 PIG
15	634	78.1	192	2	Q9SM33 FELCA
16	633	78.0	192	2	Q865B8 FELCA
17	626	77.1	192	2	Q9N1P7 SUS
18	613	75.5	193	1	IL18 CANFA
19	578	71.2	177	2	Q6STL7 PIG
20	536.5	66.1	195	2	Q80Y07 MERUN
21	515	63.4	189	2	Q80SS8 MOUSE
22	515	63.4	192	1	IL18 MOUSE
23	514.5	63.4	194	1	IL18 RAT
24	511.5	63.0	194	2	Q541E6 RAT
25	501	61.7	192	2	Q6USQ6 MOUSE
26	441	54.3	196	2	Q91Z66 SIGHI
27	313	38.5	84	2	Q95LE7 CANFA
28	293	24.1	45	2	Q9NQ49 HUMAN
29	194	23.8	211	2	Q98SQ1 ANAPL
30	184.5	22.7	196	2	Q6IT44 CHICK
31	184.5	22.7	198	2	Q8AV26 MELGA

32	182.5	22.5	198	2	Q918D2 CHICK
33	178.5	22.0	196	1	IL18 CHICK
34	174.5	21.5	198	2	Q584P2 CHICK
35	116	14.3	199	2	Q70PK1 ONCMY
36	111	13.7	182	2	Q6EV48 ONCMY
37	111	13.7	199	2	Q6EV49 ONCMY
38	94.5	11.6	1408	2	Q4S1M3 TETNG
39	88.5	10.9	357	2	Q5BD42 EMENI
40	88	10.8	181	2	Q6F0J1 MESFL
41	88	10.8	4705	1	FAT2 DROME
42	86.5	10.7	376	2	Q8K4E6 MOUSE
43	86.5	10.7	376	2	Q8K4E7 MOUSE
44	86.5	10.7	1037	2	Q4N4R1 THEPA
45	85.5	10.5	867	2	Q7RNN8 PLAYO
46	85	10.5	252	2	Q8JZN4 MOUSE
47	85	10.5	381	1	SPP2 SCHPO
48	84.5	10.4	376	2	Q8K4E8 MOUSE
49	84.5	10.4	443	2	Q5AVG0 EMENI
50	84	10.3	1101	2	Q6CIC3 KLULA
51	83.5	10.3	454	2	Q8HZU5 9CHIR
52	83.5	10.3	454	2	Q8HZU6 9CHIR
53	83.5	10.3	454	2	Q8HZU7 9CHIR
54	83.5	10.3	859	2	Q55C96 DICDI
55	83	10.2	289	2	Q5ONCO ENTHI
56	83	10.2	376	2	Q8JZN0 MOUSE
57	83	10.2	654	2	Q59MA6 CANAL
58	83	10.2	664	2	Q4Z297 PLABE
59	83	10.2	748	2	Q6ZNI6 HUMAN
60	83	10.2	788	2	Q6ZMV3 HUMAN
61	82.5	10.2	268	1	IL1A LAMGL
62	82.5	10.2	319	2	Q4FLU1 PRICK
63	82.5	10.2	780	2	Q5E4J4 VIBF1
64	82	10.1	263	2	Q74316 SCHPO
65	82	10.1	1156	2	Q7RH07 PLAYO
66	82	10.1	1374	2	Q54MY6 DICDI
67	82	10.1	1534	2	Q8MPV7 CAEEL
68	81.5	10.0	270	1	IL1A PIG
69	81.5	10.0	599	2	Q8I2G6 PLAF7
70	81.5	10.0	617	2	Q25986 PLAF7
71	81.5	10.0	1049	2	Q93KFO 9FIRM
72	81	10.0	264	2	Q5HD69 STAAC
73	81	10.0	267	1	IL1A RABIT
74	81	10.0	1085	2	Q6BMT0 DEBHA
75	80.5	9.9	825	2	Q8IC17 PLAF7
76	80.5	9.9	866	2	Q84500 CHLTR
77	80	9.9	1449	1	DPO3 CLOPE
78	80	9.9	1868	2	Q6BNV2 DEBHA
79	79.5	9.8	247	2	Q61OH0 CAEBR
80	79.5	9.8	522	2	Q5U508 XENLA
81	79.5	9.8	595	2	Q9SDM4 DUNTE
82	79.5	9.8	664	1	DNAK CHLCV
83	79.5	9.8	1044	2	Q94173 PNECA
84	79	9.7	425	1	Q4Z7S9 PLABE
85	79	9.7	452	1	PCRA HELPY
86	79	9.7	925	2	Q4YV66 PLABE
87	79	9.7	1017	2	Q54AZ4 DICDI
88	79	9.7	10578	2	Q8ISF5 CAEEL
89	79	9.7	18519	2	Q8ISF6 CAEEL
90	79	9.7	18534	2	Q8ISF7 CAEEL
91	78.5	9.7	204	2	Q9ZNI7 CLOHI
92	78.5	9.7	396	2	Q5XVE2 ARATH
93	78.5	9.7	420	2	Q5AGB9 CANAL
94	78.5	9.7	570	2	Q5CJX1 CRYHO
95	78.5	9.7	578	2	Q5CWL8 CRYPV
96	78.5	9.7	731	2	Q4YVY1 PLABE
97	78.5	9.7	1061	2	Q8DU02 STRMU
98	78.5	9.7	1518	2	Q512B0 ENTHI
99	78	9.6	261	2	Q7NAD8 MYCGA
100	78	9.6	261	2	Q8CU21 STAEP

ALIGNMENTS

```

RESULT 1
ID Q6WJ7 HUMAN PRELIMINARY; PRT; 189 AA.
AC Q6WJ7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DELTA3PRO-IL-18.
GN Name=IL18;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaggero A., De Ambrosis A., Mezzanzanica D., Piazza T., Rubartelli A.,
RA Figini M., Canevari S., Ferrini S.;
RT "A novel isoform of pro-interleukin-18 expressed in ovarian tumors is
RT resistant to caspase-1 and -4 processing.";
RL Oncogene 0:0-0(2004).
DR EMBL: AY266351; AAP92112.1; -; mRNA.
DR SMR; Q6WJ7; 33-189.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
SQ SEQUENCE 189 AA; 21896 MW; A8BA275CF713A4B6 CRC64;

Query Match 99.9%; Score 811; DB 2; Length 189;
Best Local Similarity 99.4%; Pred. No. 3.9e-68;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLVIRNLNDQVLFIDQGNPLFEDMTSDCRNAPRTFIISMYKDSQPRGM 60
DB 33 YFGKLESKLVIRNLNDQVLFIDQGNPLFEDMTSDCRNAPRTFIISMYKDSQPRGM 92
QY 61 AVTISVCKEKLXLSCKENKIISFKEMPPDNKIDKSDIIFQFORSVPGHDKMKQFESSY 120
DB 93 AVTISVCKEKLXLSCKENKIISFKEMPPDNKIDKSDIIFQFORSVPGHDKMKQFESSY 152
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 153 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 189

RESULT 2
IL18 HUMAN
ID IL18 HUMAN STANDARD; PRT; 193 AA.
AC Q14116; O75599;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN Name=IL18; Synonyms=IGIF, IL1F4;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Liver;
RX MEDLINE=96247646; PubMed=8666798;
RA Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
RA Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,
RA Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
RT "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
RT in Escherichia coli, and studies on the biologic activities of the
RT protein.";
RL J. Immunol. 156:4274-4279 (1996).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].

```

Yong D., Guixin D., Lihua H., Haitao W.;  
 "Cloning and sequencing of the cDNA for precursor hIL-18.";  
 Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 [3]  
 NUCLEOTIDE SEQUENCE [MRNA].  
 RA Liu J., Peng X., Yuan J., Qiang B.;  
 RP "Cloning of human interleukin 18 cDNA.";  
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TISSUE=Urinary bladder;  
 RX MEDLINE=232388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Rahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
 RA Schemm A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 NUCLEOTIDE SEQUENCE OF 2-193.  
 RC TISSUE=PerIPHERAL blood;  
 RA Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Augments natural killer cell activity in spleen cells  
 CC and stimulates interferon gamma production in T helper type 1  
 CC cells.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-1 family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL: D49950; BAA08706.1; -; mRNA.  
 CC EMBL: AF077611; AAC27787.1; -; mRNA.  
 CC EMBL: AY044641; AAK95950.1; -; mRNA.  
 CC EMBL: BC007007; AAH07007.1; -; mRNA.  
 CC EMBL: BC007461; AAH07461.1; -; mRNA.  
 CC EMBL: U90434; AAB50010.1; -; mRNA.  
 CC PDB: 1JOS; NMR: A-37-193.  
 CC OGP: Q14116; -;  
 CC Ensembl: ENSG00000150782; Homo sapiens.  
 CC HGNC: HGNC:5986; IL18.  
 CC H-InvDB: HIX0010123; -;  
 CC MIM: 600953; -;  
 CC GO: GO:0005576; C:extracellular region; TAS.  
 CC GO: GO:0005125; F:cytokine activity; TAS.  
 CC GO: GO:0004871; F:signal transducer activity; TAS.  
 CC GO: GO:0001525; P:angiogenesis; IDA.  
 CC GO: GO:0007267; P:cell-cell signaling; TAS.  
 CC GO: GO:0042033; P:chemokine biosynthesis; TAS.  
 CC GO: GO:0042253; P:granulocyte macrophage colony-stimulating f...; TAS.  
 CC GO: GO:0006955; P:immune response; TAS.  
 CC GO: GO:0042095; P:induction of apoptosis via death domain rec...; ISS.  
 CC GO: GO:0008625; P:induction of interferon-gamma biosynthesis; TAS.  
 CC GO: GO:0042231; P:interleukin-13 biosynthesis; TAS.  
 CC GO: GO:0042094; P:interleukin-2 biosynthesis; TAS.



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DR GO: 0042104; P: positive regulation of activated T cell pro. . . ; IDA.
DR GO: 0030155; P: regulation of cell adhesion; IDA.
DR GO: 0030431; P: sleep; ISS.
DR GO: 0042092; P: T-helper 2 type immune response; TAS.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
KW 3D-structure; Cytokine.
FT PROPEP 1 36
FT CHAIN 37 193
FT CONFLICT 66 66
FT CONFLICT 86 86
FT CONFLICT 86 86
FT CONFLICT 191 191
SQ SEQUENCE 193 AA; 22326 MW; 323C62C203788D55 CRC64;

Query Match 99.9%; Score 811; DB 1; Length 193;
Best Local Similarity 99.4%; Pred. NO. 4e-68;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 96

QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSKDIIFQFQSVPGHDKMKQFESSY 120
DB 97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTSKDIIFQFQSVPGHDKMKQFESSY 156

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 3
Q6FGY3_HUMAN
ID Q6FGY3_HUMAN PRELIMINARY; PRT; 193 AA.
AC Q6FGY3;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE IL18 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schattner R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.,
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR541973; CAG46771.1; -. mRNA.
DR EMBL; CR542001; CAG46798.1; -. mRNA.
SQ SEQUENCE 193 AA; 22326 MW; 323C62C203788D55 CRC64;

Query Match 99.9%; Score 811; DB 2; Length 193;
Best Local Similarity 99.4%; Pred. NO. 4e-68;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 96

QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSKDIIFQFQSVPGHDKMKQFESSY 120
DB 97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTSKDIIFQFQSVPGHDKMKQFESSY 156

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193
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RESULT 4
Q96KJ8_HUMAN
ID Q96KJ8_HUMAN PRELIMINARY; PRT; 193 AA.
AC Q96KJ8;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Interleukin 18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ying P., Jianxin L.,
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF380360; AAK57024.1; -. mRNA.
DR HSSP; Q14116; LJ08.
DR SMR; Q96KJ8; 37-193.
DR GO: 0005576; C: extracellular region; IEA.
DR GO: 0005149; F: interleukin-1 receptor binding; IEA.
DR GO: 0006955; P: immune response; IEA.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;

Query Match 98.3%; Score 798; DB 2; Length 193;
Best Local Similarity 97.5%; Pred. NO. 6.7e-67;
Matches 153; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 96

QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSKDIIFQFQSVPGHDKMKQFESSY 120
DB 97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTSKDIIFQFQSVPGHDKMKQFESSY 156

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 5
Q9BG15_MACMU
ID Q9BG15_MACMU PRELIMINARY; PRT; 193 AA.
AC Q9BG15;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Interleukin-18.
GN Name=IL18;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheciidae; Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE; 21229850; PubMed=11331040; DOI=10.1089/107999001750133212;
RA Glavedoni L.D., Imhoof J.D., Parodi L.M., Velasquillo C.M.,
RA Hodara V.L.;
RT "Expression of the interleukin-18 gene from rhesus macaque by the
RT simian immunodeficiency virus does not result in increased viral
RT replication.";
RL J. Interferon Cytokine Res. 21:173-180(2001).
DR EMBL; AF303732; AAK13416.1; -. mRNA.
DR HSSP; Q14116; LJ08.
DR SMR; Q9BG15; 37-193.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
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SQ SEQUENCE 193 AA; 22325 MW; B2B2D29C033BB0B5E CRC64;
Query Match
Best Local Similarity 97.5%; Score 792; DB 2; Length 193;
Matches 150; Conservative .5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFILSMYKDSQPRGM 60
Dy 37 YFGKLESKLSIIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFILSMYKDSQPRGM 96

Qy 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNKTKSDIIFQFQSVPGHDKMKQFESSY 120
Dy 97 AVAISVCKEIKSLSCENKIISFKEMNPPDNKTKSDIIFQFQSVPGHDKMKQFESSY 156

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Dy 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 6
IL18_HORSE
ID Q9XSO7; STANDARD; PRT; 193 AA.
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma)
GN Name=IL18; Synonyms=IGIF;
OS Equus caballus (Horse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Argyle D.J., Onions D.E.;
RA Nicolson L., Penha-Goncalves M.N., Keanie J.L., Logan N.A.;
RA Argyle D.J., Onions D.E.;
RT "Nucleotide sequence of equine interleukin 12 and 18 cDNAs.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Augments natural killer cell activity in spleen cells
CC and stimulates interferon gamma production in T helper type I
CC cells (by similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; Y11131; CAA72013.1; -; mRNA.
DR SMR; Q9XSO7; 37-193.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
KW Cytokine.
FT PROPEP 1 36 By similarity.
FT CHAIN 37 193 Interleukin-18.
SQ SEQUENCE 193 AA; 22058 MW; 4D81535E9004ECAF CRC64;

Query Match
Best Local Similarity 81.2%; Score 659; DB 1; Length 193;
Matches 122; Conservative 21; Mismatches 14; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFILSMYKDSQPRGM 60
Dy 37 YFGKLESKLSIIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFILSMYKDSQPRGM 96

Qy 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNKTKSDIIFQFQSVPGHDKMKQFESSY 120
Dy 97 AVTISVCKEIKSLSCENKIISFKEMNPPDNKTKSDIIFQFQSVPGHDKMKQFESSY 156

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Dy 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

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Db 157 KGYFLACEKENDLFKILKKEDEGDKSVMTVQNON 193

RESULT 7
Q6TLW4_BUBBU
ID Q6TLW4_BUBBU PRELIMINARY; PRT; 193 AA.
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interleukin 18.
GN Name=IL18;
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chaudhury P., Bera B.C.;
RA "Cloning and sequencing of Indian water buffalo interleukin-18 cDNA.";
RL Eur. J. Immunogenet. 32:75-78(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Chaudhuri P., Bera B.C.;
RA Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AX394479; AAQ94552.1; -; mRNA.
DR SMR; Q6TLW4; 37-193.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR PIR; P00340; IL1; 1.
SQ SEQUENCE 193 AA; 22176 MW; 66116F198DE94BC4 CRC64;

Query Match
Best Local Similarity 81.2%; Score 659; DB 2; Length 193;
Matches 122; Conservative 22; Mismatches 13; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFILSMYKDSQPRGM 60
Dy 37 HFGKLEPKLSIIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFILSMYKDSQPRGM 96

Qy 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNKTKSDIIFQFQSVPGHDKMKQFESSY 120
Dy 97 AVTISVCKEIKSLSCENKIISFKEMNPPDNKTKSDIIFQFQSVPGHDKMKQFESSY 156

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Dy 157 KGYFLACEKENDLFKILKKEDEGDKSVMTVQNON 193

RESULT 8
Q6T573_BUBBU
ID Q6T573_BUBBU PRELIMINARY; PRT; 193 AA.
AC Q6T573;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interleukin-18.
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Premraj A., Sreekumar E., Rasool T.J.;
RA Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436506; AAR29081.1; -; mRNA.
DR SMR; Q6T573; 37-193.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000975; Interleukin_1.

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DR Pfam; PF00340; IL1; 1.  
SQ SEQUENCE 193 AA; 22190 MW; 93103E5C62B745DE CRC64;  
Query Match 81.2%; Score 659; DB 2; Length 193;  
Best Local Similarity 77.1%; Pred. No. 7.9e-54;  
Matches 122; Conservative 22; Mismatches 13; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSCDRDNAPRTIFIIISMYKDSQPRGM 60  
DB 37 HFGKLEPKLSIIRNLNDQVLFINQGNQPVFEDMPDSDCSNAPQTIFIIYMYKDSLTRL 96  
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQSVPGHDKNMQFESSY 120  
DB 97 AVTISVQCKMSTLSCENKIVSFKEMNPPDNIDNEGSIIIFQSVPGHDDKIQFESSLY 156  
QY 121 EGYFLACEKRDLPFLILKKEDELGRSIMFTVQNE 157  
DB 157 KGYFLACKENDLPFLILKQDDNGDKSVMTVQON 193

## RESULT 9

Q9MZL8\_BOVIN PRELIMINARY; PRT; 178 AA.  
ID Q9MZL8\_BOVIN  
AC Q9MZL8;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Interleukin-18 (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Kidney;  
RA Olsen S.C., Lee I.K., Mwangi S.M., Kehrli M., Bolin C.A.;  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF173175; AAF89833.1; -, mRNA.  
DR HSP; Q14116; IJOS.  
DR SMR; Q9MZL8; 22-178.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR000975; Interleukin\_1.  
DR Pfam; PF00340; IL1; 1.  
DR SMART; SM00125; IL1; 1.  
DR NON\_TER 178 178  
FT NON\_TER  
SQ SEQUENCE 178 AA; 20631 MW; 815D6B2B88ACB497 CRC64;

Query Match 80.5%; Score 654; DB 2; Length 178;  
Best Local Similarity 77.1%; Pred. No. 2.1e-53;  
Matches 121; Conservative 23; Mismatches 13; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSCDRDNAPRTIFIIISMYKDSQPRGM 60  
DB 22 HFGKLEPKLSIIRNLNDQVLFINQGNQPVFEDMPDSDCSNAPQTIFIIYMYKDSLTRL 81  
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQSVPGHDKNMQFESSY 120  
DB 82 AVTISVQCKMSTLSCENKIVSFKEMNPPDNIDNEGSIIIFQSVPGHDDKIQFESSLY 141  
QY 121 EGYFLACEKRDLPFLILKKEDELGRSIMFTVQNE 157  
DB 142 KGYFLACKENDLPFLILKQDDNDRKSVMTVQON 178

## RESULT 10

IL18\_BOVIN  
ID IL18\_BOVIN  
AC Q9TU73;  
DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor) (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).  
GN Name=IL18;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20012648; PubMed=10547157; DOI=10.1089/1079990999313118;  
RA Shoda L.K., Zarling D.S., Hirano A., Brown W.C.;  
RT "Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-18 expression in macrophages and its IFN-gamma-inducing activity.";  
RL J. Interferon Cytokine Res. 19:1169-1177(1999).  
CC -!- FUNCTION: Augments natural killer cell activity in spleen cells and stimulates interferon gamma production in T helper type 1 cells (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the IL-1 family.  
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DR EMBL; AF124789; AAF08686.1; -, mRNA.  
DR SMR; Q9TU73; 37-193.  
DR InterPro; IPR000975; Interleukin\_1.  
DR Pfam; PF00340; IL1; 1.  
DR SMART; SM00125; IL1; 1.  
KW Cytokine.  
FT PROPEP 1 36 By similarity.  
FT CHAIN 37 193 Interleukin-18.  
SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;  
Query Match 80.5%; Score 654; DB 1; Length 193;  
Best Local Similarity 77.1%; Pred. No. 2.3e-53;  
Matches 121; Conservative 23; Mismatches 13; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSCDRDNAPRTIFIIISMYKDSQPRGM 60  
DB 37 HFGKLEPKLSIIRNLNDQVLFINQGNQPVFEDMPDSDCSNAPQTIFIIYMYKDSLTRL 96  
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQSVPGHDKNMQFESSY 120  
DB 97 AVTISVQCKMSTLSCENKIVSFKEMNPPDNIDNEGSIIIFQSVPGHDDKIQFESSLY 156  
QY 121 EGYFLACEKRDLPFLILKKEDELGRSIMFTVQNE 157  
DB 157 KGYFLACKENDLPFLILKQDDNDRKSVMTVQON 193  
RESULT 11  
Q5I931\_BOSTR PRELIMINARY; PRT; 193 AA.  
ID Q5I931\_BOSTR  
AC Q5I931;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Interleukin-18.  
OS Boselaphus tragocamelus (Nilgai).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Bovinae; Boselaphus.  
OX NCBI\_TaxID=9917;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Saini M., Swarup D., Yadav M.P., Singh G.R., Arora B.M., Chandra P., Das D.K., Gupta P.K.;

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RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY842499; AAW34191.1; -, mRNA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
SQ SEQUENCE 193 AA; 22130 MW; 75B6671696EE4A8D CRC64;

Query Match 80.2%; Score 651; DB 2; Length 193;
Best Local Similarity 77.6%; Pred. No. 4.5e-53;
Matches 121; Conservative 21; Mismatches 14; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIIFIISMYKDSQPRGM 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
37 HFGKLEPKLSIIRNLNDQVLFINGNQPVFEDMPDSCPNAPQTIIFIYMYKDSLTRL 96
QY 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNKDTKSDIIFQFQSVPGHDKMKQFESSY 120
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
97 AVTISVQCKMSTLSCENKIVSFKEMNPPDNIDNEGSDIIFQFQSVPGHDKMKQFESSLY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 156
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
157 KGFLACKENDLFKLILKQDDNGDKSVTFTVQNQ 192

RESULT 12
Q9GL09_SHEEP PRELIMINARY; PRT; 193 AA.
AC Q9GL09;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DR EMBL; AJ401033; CAC09326.2; -, mRNA.
DR HSP; Q14116; 1J08.
DR SMR; Q9GL09; 37-193.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 193 AA; 22166 MW; CCD0A329062EF18C CRC64;

Query Match 79.8%; Score 648; DB 2; Length 193;
Best Local Similarity 77.7%; Pred. No. 8.5e-53;
Matches 122; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIIFIISMYKDSQPRGM 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
37 HFGKLEPKLSIIRNLNDQVLFISQGNQPVFEDMPDSCDNAPQTIIFIYMYKDSLTRL 96
QY 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNKDTKSDIIFQFQSVPGHDKMKQFESSY 120
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
97 AVTISVQCKMSTLSCENKIVSFKEMNPPDNIDNEGSDIIFQFQSVPGHDKMKQFESSLY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
157 KGFLACKENDLFKLILKQDDNRDKSIMFTVQKN 193

RESULT 13
Q6QVC4_CAPHI
ID Q6QVC4_CAPHI PRELIMINARY; PRT; 159 AA.
AC Q6QVC4;

Query Match 79.7%; Score 647; DB 2; Length 159;
Best Local Similarity 77.1%; Pred. No. 8.4e-53;
Matches 121; Conservative 21; Mismatches 15; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIIFIISMYKDSQPRGM 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3 HFGKLEPKLSIIRNLNDQVLFISQGNQPVFEDMPDSCDNAPQTIIFIYMYKDSLTRL 62
QY 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNKDTKSDIIFQFQSVPGHDKMKQFESSY 120
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 AVTISVQCKMSTLSCENKIVSFKEMNPPDNIDNEGSDIIFQFQSVPGHDKMKQFESSLY 122
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
123 KGFLACKENDLFKLILKQDDNRDKSIMFTVQKN 159

RESULT 14
IL18_PIG STANDARD; PRT; 192 AA.
AC Q19073;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN Name=IL18; Synonyms=IGIF;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Foss D.L., Murtough M.P.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]_
RP NUCLEOTIDE SEQUENCE.
RA Penha-Goncalves M.N., Logan N.A., Nicolson L., Onions D.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [3]_
RP NUCLEOTIDE SEQUENCE.
RA Muneta Y., Mori Y.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]_
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=20260994; PubMed=10803849; DOI=10.1007/s002510050630;
RA Fournout S., Dozois C.M., Yerle M., Pinton P., Fairbrother J.M.,
RA Oswald E., Oswald I.P.;
RA "Cloning, chromosomal location, and tissue expression of the gene for
```

RT pig interleukin-18.";  
 RL Immunogenetics 51:358-365(2000).  
 CC -!- FUNCTION: Augments natural killer cell activity in spleen cells  
 CC and stimulates interferon gamma production in T helper type I  
 CC cells (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-1 family.  
 CC -----  
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 CC -----  
 DR EMBL; U68701; AAC18415.1; -; mRNA.  
 DR EMBL; Y11132; CAA72014.1; -; mRNA.  
 DR EMBL; AB010003; BAA24135.1; -; mRNA.  
 DR EMBL; AF191088; AAF71200.1; -; mRNA.  
 DR SMR; O19073; 36-192.  
 DR GO; GO:0005576; C:extracellular region; ISS.  
 DR GO; GO:0005125; F:cytokine activity; IMP.  
 DR GO; GO:0001525; P:angiogenesis; ISS.  
 DR GO; GO:0042033; P:chemokine biosynthesis; ISS.  
 DR GO; GO:0008625; P:induction of apoptosis via death domain rec. .; IDA.  
 DR GO; GO:0042095; P:interferon-gamma biosynthesis; IDA.  
 DR GO; GO:0042104; P:positive regulation of activated T cell pro. .; ISS.  
 DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR Pfam; PF00340; IL1; 1.  
 DR SMART; SM00125; IL1; 1.  
 KW Cytokine.  
 FT PROPEP 1 35 By similarity.  
 FT CHAIN 36 192 Interleukin-18.  
 SQ SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;

Query Match 78.4%; Score 637; DB 1; Length 192;  
 Best Local Similarity 75.2%; Pred. No. 9.2e-52;  
 Matches 118; Conservative 24; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFITISMYKDSQPRGM 60  
 DB 36 YFGKLEPKLSIIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFITISMYKDSLTREL 95  
 QY 61 AVTISVCKEKISXLSCKNKIISFKEMPPDNKTKSDIIFQSVPGHNDKMOFESSY 120  
 DB 96 AVTISVCKKASTLSCKNKIISFKEMSPDNIDDEGNDIIFQSVPGHDDKIQFESSLY 155  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
 DB 156 KGYFLACKENDLFKLILKKEDECGDKSIMFTVQKN 192

RESULT 15  
 Q95M33\_FELCA PRELIMINARY; PRT; 192 AA.  
 AC Q95M33;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)  
 DE Interferon-gamma inducing factor (IL-18).  
 GN Name=IGIF;  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;  
 OC Felis.  
 OC NCBI\_TaxID=9685;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hanton L., McGillivray C.P., Argyle D.J.A., Nicolson L., Onions D.E.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Qiao J., Xia X., Yang S.;

"Cloning and sequence analysis of feline IL-18 gene.";  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Y13923; CAC42918.1; -; mRNA.  
 DR EMBL; DQ100372; AAY96319.1; -; mRNA.  
 DR HSSP; Q14116; LJOS.  
 DR SMR; Q95M33; 36-192.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR Pfam; PF00340; IL1; 1.  
 SQ SEQUENCE 192 AA; 22068 MW; 5878C3DAC7A43358 CRC64;

Query Match 78.1%; Score 634; DB 2; Length 192;  
 Best Local Similarity 76.4%; Pred. No. 1.8e-51;  
 Matches 120; Conservative 21; Mismatches 16; Indels 0; Gaps 0;  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFITISMYKDSQPRGM 60  
 DB 36 YFGKLEHLKLSIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFITISMYKDSLTREL 95  
 QY 61 AVTISVCKEKISXLSCKNKIISFKEMPPDNKTKSDIIFQSVPGHNDKMOFESSY 120  
 DB 96 AVTISVNYKTMSTLSCKNKIISFKEMSPDESINDEGNDIIFQSVPGHDDKIQFESSLY 155  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
 DB 156 KGYFLACEKEKDLFKLILKKEDEGDKSIMFTVQKN 192

Search completed: January 30, 2006, 08:40:13  
 Job time : 166 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2006, 08:41:09 ; Search time 31 Seconds

(without alignments)  
54.844 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDELGDRSIMFTVQNEED 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:\*

1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	811	99.9	157	6	US-10-401-386B-64
2	805	99.1	157	6	US-10-401-386B-76
3	803	98.9	157	6	US-10-401-386B-78
4	799	98.4	157	6	US-10-401-386B-70
5	798	98.3	157	6	US-10-401-386B-66
6	798	98.3	157	6	US-10-401-386B-80
7	795	97.9	157	6	US-10-401-386B-68
8	792	97.5	157	6	US-10-401-386B-72
9	86.5	10.7	376	7	US-11-012-762-22
10	86.5	10.7	376	7	US-11-012-762-24
11	85	10.5	252	7	US-11-012-762-14
12	84.5	10.4	376	7	US-11-012-762-20
13	83	10.2	376	7	US-11-012-762-10
14	83	10.2	376	7	US-11-012-762-16
15	83	10.2	376	7	US-11-012-762-40
16	74.5	9.2	376	7	US-11-012-762-18
17	74.5	9.2	467	7	US-11-127-817-15
18	74	9.1	261	6	US-10-793-626-584
19	74	9.1	261	6	US-10-793-626-982
20	70	8.6	2668	7	US-11-124-368A-214
21	70	8.6	2668	7	US-11-124-368A-215
22	66.5	8.2	614	7	US-11-150-845-34
23	64.5	7.9	414	6	US-10-631-558-2
24	64	7.9	619	6	US-10-517-939-352
25	63.5	7.8	479	6	US-10-517-939-350

Sequence 397, App  
Sequence 3298, App  
Sequence 776, App  
Sequence 672, App  
Sequence 46, Appli  
Sequence 1, Appli  
Sequence 84, Appli  
Sequence 557, App  
Sequence 3218, App  
Sequence 330, App  
Sequence 14, Appli  
Sequence 1056, App  
Sequence 6, Appli  
Sequence 20, Appli  
Sequence 4, Appli  
Sequence 2, Appli  
Sequence 1121, App  
Sequence 1134, App  
Sequence 1136, App  
Sequence 1142, App  
Sequence 1132, App  
Sequence 12, Appli  
Sequence 3, Appli  
Sequence 171, App  
Sequence 187, App  
Sequence 31, Appli  
Sequence 572, App  
Sequence 576, App  
Sequence 578, App  
Sequence 568, App  
Sequence 82, Appli  
Sequence 570, App  
Sequence 28, Appli  
Sequence 580, App  
Sequence 600, App  
Sequence 594, App  
Sequence 5, Appli  
Sequence 586, App  
Sequence 592, App  
Sequence 602, App  
Sequence 2, Appli  
Sequence 5510, App  
Sequence 1648, App  
Sequence 2364, App  
Sequence 566, App  
Sequence 1478, App  
Sequence 36, Appli  
Sequence 54, Appli  
Sequence 52, Appli  
Sequence 145, App  
Sequence 144, App  
Sequence 24, Appli  
Sequence 533, App  
Sequence 3256, App  
Sequence 68, Appli  
Sequence 130, App  
Sequence 154, App  
Sequence 262, App  
Sequence 1436, App  
Sequence 36, Appli  
Sequence 43, Appli  
Sequence 111, App  
Sequence 51, App  
Sequence 195, App  
Sequence 9, Appli  
Sequence 1059, App  
Sequence 2, Appli  
Sequence 6, Appli  
Sequence 953, App  
Sequence 5, Appli  
Sequence 119, App  
Sequence 8, Appli  
Sequence 11, Appli

Sequence 1346, Ap  
Sequence 6, Appli

## ALIGNMENTS

<b>RESULT 1</b>					
US-10-401-386B-64	; Sequence 64, Application US/10401386B				
;	Publication No. US20050261213A1				
;	GENERAL INFORMATION:				
;	APPLICANT: Patrick Branigan				
;	APPLICANT: Theresa J Goletz				
;	APPLICANT: David M Knight				
;	APPLICANT: Stephen G McCarthy				
;	APPLICANT: Bernard J Scallion				
;	APPLICANT: Linda A Snyder				
;	TITLE OF INVENTION: Nucleic Acid Compositions and Methods				
;	FILE OF INVENTION: for Use				
;	FILE REFERENCE: CEN 310CIP				
;	CURRENT APPLICATION NUMBER: US/10/401,386B				
;	CURRENT FILING DATE: 2003-03-28				
;	PRIOR APPLICATION NUMBER: 10/247,203				
;	PRIOR FILING DATE: 2002-09-19				
;	PRIOR APPLICATION NUMBER: 60/328,371				
;	PRIOR FILING DATE: 2001-10-10				
;	NUMBER OF SEQ ID NOS: 81				
;	SOFTWARE: FastSeq for Windows Version 4.0				
;	SEQ ID NO 64				
;	LENGTH: 157				
;	TYPE: PRT				
;	ORGANISM: Homo sapiens				
US-10-401-386B-64					
Query Match            99.9%; Score 811; DB 6; Length 157;					
Best Local Similarity   99.4%; Pred.No.2.3e-80;					
Matches 156; Conservative 1; Mismatches 1; Indels 0; Gaps 0;					
Qy	1 YFGKLESKLSVIRNLNDQVLFDGCRNRPFLFEDMTDSDCRDNAPRTIFIISMYKDSQPGRM 60				
Db	1 YFGKLESKLSVIRNLNDQVLFDGCRNRPFLFEDMTDSDCRDNAPRTIFIISMYKDSQPGRM 60				
Qy	61 AVTTSVCKEKSIXLSCENKIISFKEMNPDDNIKOTKSDIIIFQRSPVGHDKNMQPFESSY 120				
Db	61 AVTTSVCKEKISTLSCENKIISFKEMNPDDNIKOTKSDIIIFQRSPVGHDKNMQPFESSY 120				
Qy	121 EGYFLACEKERDLFKLLIKKEDELGDRSIMFTVQNED 157				
Db	121 EGYFLACEKERDLFKLLIKKEDELGDRSIMFTVQNED 157				
<b>RESULT 2</b>					
US-10-401-386B-76	; Sequence 76, Application US/10401386B				
;	Publication No. US20050261213A1				
;	GENERAL INFORMATION:				
;	APPLICANT: Patrick Branigan				
;	APPLICANT: Theresa J Goletz				
;	APPLICANT: David M Knight				
;	APPLICANT: Stephen G McCarthy				
;	APPLICANT: Bernard J Scallion				
;	APPLICANT: Linda A Snyder				
;	TITLE OF INVENTION: Nucleic Acid Compositions and Methods				
;	FILE OF INVENTION: for Use				
;	FILE REFERENCE: CEN 310CIP				
;	CURRENT APPLICATION NUMBER: US/10/401,386B				
;	CURRENT FILING DATE: 2003-03-28				
;	PRIOR APPLICATION NUMBER: 10/247,203				
;	PRIOR FILING DATE: 2002-09-19				
;	PRIOR APPLICATION NUMBER: 60/328,371				
;	PRIOR FILING DATE: 2001-10-10				
;	NUMBER OF SEQ ID NOS: 81				

	Qy	1	YFGKLESKLSVIRNLNDQVLFDIQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM	60	
	Dd	1	YFGKLESKLSVIRNLNNQVLFDIQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM	60	
	Qy	61	AVTISVKCEKISXLSKENKIISFKEMNPPDNIKDTKSIDIIFQRSVPGHDKMQPESSESSY	120	
	Dd	61	AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSIDIIFQRSVPGHDKMQPESSESSY	120	
	Qy	121	EGYFLACEKERDLFKLIILKEDELGDRSIMFTVQNED	157	
	Dd	121	EGYFLTCERKERDLFKLIILKEDELGDRSIMFTVQNED	157	
	RESULT 6				
	US-10-401-386B-80				
	; Sequence 80, Application US/10401386B				
	; Publication No. US20050261213A1				
	; GENERAL INFORMATION:				
	; APPLICANT: Patrick Branigan				
	; APPLICANT: Theresa J Goletz				
	; APPLICANT: David M Knight				
	; APPLICANT: Stephen G McCarthy				
	; APPLICANT: Bernard J Scallan				
	; APPLICANT: Linda A Snyder				
	; TITLE OF INVENTION: Nucleic Acid Compositions and Methods				
	; FILE REFERENCE: CEN 310CIP				
	; CURRENT APPLICATION NUMBER: US/10/401,386B				
	; PRIOR FILING DATE: 2003-03-28				
	; PRIOR APPLICATION NUMBER: 10/247,203				
	; PRIOR FILING DATE: 2002-09-19				
	; PRIOR APPLICATION NUMBER: 60/328,371				
	; PRIOR FILING DATE: 2001-10-10				
	; NUMBER OF SEQ ID NOS: 81				
	; SOFTWARE: FastSeq for Windows Version 4.0				
	; SEQ ID NO 80				
	; LENGTH: 157				
	; TYPE: PRT				
	; ORGANISM: Homo sapiens				
	US-10-401-386B-80				
	Query Match 98.3%; Score 798; DB 6; Length 157;				
	Best Local Similarity 97.5%; Pred. No. 5.6e-79;				
	Matches 153; Conservative 2; Mismatches 2; Indels 0; Gaps 0				
	Qy	1	YFGKLESKLSVIRNLNDQVLFDIQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM	60	
	Dd	1	YFGKLESKLTIVIRNLNNQVLFDIQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM	60	
	Qy	61	AVTISVKCEKISXLSKENKIISFKEMNPPDNIKDTKSIDIIFQRSVPGHDKMQPESSESSY	120	
	Dd	61	AVAISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSIDIIFQRSVPGHDKMQPESSESSY	120	
	Qy	121	EGYFLACEKERDLFKLIILKEDELGDRSIMFTVQNED	157	
	Dd	121	EGYFLACEKERDLFKLIILKEDELGDRSIMFTVQNED	157	
	RESULT 7				
	US-10-401-386B-68				
	; Sequence 68, Application US/10401386B				
	; Publication No. US20050261213A1				
	; GENERAL INFORMATION:				
	; APPLICANT: Patrick Branigan				
	; APPLICANT: Theresa J Goletz				
	; APPLICANT: David M Knight				
	; APPLICANT: Stephen G McCarthy				
	; APPLICANT: Bernard J Scallan				
	; APPLICANT: Linda A Snyder				
	; TITLE OF INVENTION: Nucleic Acid Compositions and Methods				
	; FILE REFERENCE: CEN 310CIP				
	; CURRENT APPLICATION NUMBER: US/10/401,386B				
	; PRIOR FILING DATE: 2003-03-28				
	; PRIOR APPLICATION NUMBER: 10/247,203				
	; PRIOR FILING DATE: 2002-09-19				
	; PRIOR APPLICATION NUMBER: 60/328,371				
	; PRIOR FILING DATE: 2001-10-10				
	; NUMBER OF SEQ ID NOS: 81				
	; SOFTWARE: FastSeq for Windows Version 4.0				
	; SEQ ID NO 66				
	; LENGTH: 157				
	; TYPE: PRT				
	; ORGANISM: Homo sapiens				
	US-10-401-386B-66				
	Query Match 98.3%; Score 798; DB 6; Length 157;				
	Best Local Similarity 97.5%; Pred. No. 5.6e-79;				
	Matches 153; Conservative 2; Mismatches 2; Indels 0; Gaps 0				
	RESULT 5				
	US-10-401-386B-66				
	; Sequence 66, Application US/10401386B				
	; Publication No. US20050261213A1				
	; GENERAL INFORMATION:				
	; APPLICANT: Patrick Branigan				
	; APPLICANT: Theresa J Goletz				
	; APPLICANT: David M Knight				
	; APPLICANT: Stephen G McCarthy				
	; APPLICANT: Bernard J Scallan				
	; APPLICANT: Linda A Snyder				
	; TITLE OF INVENTION: Nucleic Acid Compositions and Methods				
	; FILE REFERENCE: CEN 310CIP				
	; CURRENT APPLICATION NUMBER: US/10/401,386B				
	; PRIOR FILING DATE: 2003-03-28				
	; PRIOR APPLICATION NUMBER: 10/247,203				
	; PRIOR FILING DATE: 2002-09-19				
	; PRIOR APPLICATION NUMBER: 60/328,371				
	; PRIOR FILING DATE: 2001-10-10				
	; NUMBER OF SEQ ID NOS: 81				
	; SOFTWARE: FastSeq for Windows Version 4.0				
	; SEQ ID NO 66				
	; LENGTH: 157				
	; TYPE: PRT				
	; ORGANISM: Homo sapiens				
	US-10-401-386B-66				
	Query Match 98.3%; Score 798; DB 6; Length 157;				
	Best Local Similarity 97.5%; Pred. No. 5.6e-79;				
	Matches 153; Conservative 2; Mismatches 2; Indels 0; Gaps 0				



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; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-68

Query Match          97.5%; Score 795; DB 6; Length 157;
Best Local Similarity 97.5%; Pred. No. 1.2e-78;
Matches 153; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSKCNKIISFKENMPDNIKOTKSDIIFQFORSVPGHDKNMQPESSSY 120
Db 61 AVTISVKCEKISXLSKCNKIISFKENMPDNIKOTKSDIIFQFORSVPGHDKNMQPESSSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQSED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQSED 157

RESULT 8
US-10-401-386B-72
; Sequence 72, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; TITLE OF INVENTION: for Use
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-10-401-386B-72

Query Match          97.5%; Score 792; DB 6; Length 157;
Best Local Similarity 95.5%; Pred. No. 2.5e-78;
Matches 150; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSKCNKIISFKENMPDNIKOTKSDIIFQFORSVPGHDKNMQPESSSY 120
Db 61 AVAISVKCEKISXLSKCNKIISFKENMPDNIKOTKSDIIFQFORSVPGHDKNMQPESSSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQSED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQSED 157

; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-68

Query Match          97.9%; Score 795; DB 6; Length 157;
Best Local Similarity 97.5%; Pred. No. 1.2e-78;
Matches 153; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSKCNKIISFKENMPDNIKOTKSDIIFQFORSVPGHDKNMQPESSSY 120
Db 61 AVTISVKCEKISXLSKCNKIISFKENMPDNIKOTKSDIIFQFORSVPGHDKNMQPESSSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQSED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQSED 157

RESULT 9
US-11-012-762-22
; Sequence 22, Application US/11012762
; Publication No. US20050244815A1
; GENERAL INFORMATION:
; APPLICANT: Georgia State University Research Foundation, Inc.
; TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes
; FILE REFERENCE: GSU1.PCT
; CURRENT APPLICATION NUMBER: US/11/012,762
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US03/19300
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/390,046
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-762-22

Query Match          10.7%; Score 86.5; DB 7; Length 376;
Best Local Similarity 21.6%; Pred. No. 0.052;
Matches 37; Conservative 29; Mismatches 68; Indels 37; Gaps 5;

QY 5 LESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGMVATI 64
Db 59 VKGKCTALKGRSDADLVVFLNNLTVFEDLNQ-----QGVLIKEIKKQLYEVQHERRF 111
QY 65 SVKCEKISXLSKCNKIISFKENMPDNIKOTKSDI-----IF 101
Db 112 GVKFEVQSLRSPNGRALSFK-LSAPDLLKVEKFDVLPAYDLLDHLSILKPNRQLYANLI 170
QY 102 FQRSVPGHDKNMQPESSSYEGYFLACE--KERDLFKLILK---KEDELGD 146
Db 171 SGRTPPGKDPKLSICFMGLRKRYFLNCRPTKURLRLVLTQWYQLCCKELGD 221

RESULT 10
US-11-012-762-24
; Sequence 24, Application US/11012762
; Publication No. US20050244815A1
; GENERAL INFORMATION:
; APPLICANT: Georgia State University Research Foundation, Inc.
; TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes
; FILE REFERENCE: GSU1.PCT
; CURRENT APPLICATION NUMBER: US/11/012,762
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US03/19300
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/390,046
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-762-24

Query Match          10.7%; Score 86.5; DB 7; Length 376;
Best Local Similarity 23.3%; Pred. No. 0.052;
Matches 40; Conservative 28; Mismatches 65; Indels 39; Gaps 7;

QY 5 LESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGMVATI 64
Db 59 VKGKCTALKGRSDADLVVFLNNLTVFEDLNQ-----QGVLIKEIKKQLYEVQHERRF 111
QY 65 SVKCEKISXLSKCNKIISFKENMPDNIKOTKSDI-----PFQ--- 103
```

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Db 112 GVKFEVQSLRSPNSRALSFK-LSAPDLLKEVKFDVLPAYDLDLHLNLLKPNQOQFYANLI 170
QY 104 --RSVPGHDKNQMFSSSYEGYFLACE--KERDLFKLI-----LKKEDELGD 146
Db 171 SGRTPPGKEGKLSICFMGLRKYFLNCRPTKLRLRLVTHWYQLCKE-KLGD 221

RESULT 11
US-11-012-762-14
; Sequence 14, Application US/11012762
; Publication No. US20050244815A1
; GENERAL INFORMATION:
; APPLICANT: Georgia State University Research Foundation, Inc.
; TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes
; FILE REFERENCE: GSUI.PCT
; CURRENT APPLICATION NUMBER: US/11/012,762
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US03/19300
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/390,046
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-762-14

Query Match 10.5%; Score 85; DB 7; Length 252;
Best Local Similarity 23.1%; Pred. No. 0.045; Indels 66; Gaps 8;
Matches 42; Conservative 25; Mismatches 49;

QY 3 GKLESKLSVIRN-----LNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKD 54
Db 68 GRSDADLVFLNLTSPEDQLNQGVLIKEIKQLCEVQHERRC----- 111

QY 55 SOPRGMAVTISVKCEKISXLSKSCENKIISFKEMNPPDNIKDTSKDI----- 100
Db 112 -----GVKFEVHLSRSPNSRALSFK-LSAPDLLKEVKFDVLPAYDLDLHLNLLK 160
QY 101 ----PFQ-----RSVPGHDKNQMFSSSYEGYFLACE--KERDLFKLI-----LKKEDEL 144
Db 161 PNQOQFYANLISGRTPPGKEGKLSICFMGLQKYFLNCRPTKLRLRLVTHWYQLCKE-KL 219

QY 145 GD 146
Db 220 GD 221

RESULT 12
US-11-012-762-20
; Sequence 20, Application US/11012762
; Publication No. US20050244815A1
; GENERAL INFORMATION:
; APPLICANT: Georgia State University Research Foundation, Inc.
; TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes
; FILE REFERENCE: GSUI.PCT
; CURRENT APPLICATION NUMBER: US/11/012,762
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US03/19300
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/390,046
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-762-20

Query Match 10.4%; Score 84.5; DB 7; Length 376;
```

```
Best Local Similarity 23.3%; Pred. No. 0.086;
Matches 40; Conservative 28; Mismatches 65; Indels 39; Gaps 7;

QY 5 LESKLSVIRNLDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGMVTI 64
Db 59 VKGCKTALKGRSDADLVFLNLTSPEDQLNQ-----QGVLIKEIKQLVEVQHERRF 111

QY 65 SVKCEKISXLSKSCENKIISFKEMNPPDNIKDTSKDI-----PFQ----- 103
Db 112 GVKFEVQSLRSPNSRALSFK-LSAPDLLKEVKFDVLPAYDLDLHLNLLKPNQOQFYANLI 170
QY 104 --RSVPGHDKNQMFSSSYEGYFLACE--KERDLFKLI-----LKKEDELGD 146
Db 171 SGRTPPGKEGKLLICFMGLRKYFLNCRPTKLRLRLVTHWYQLCKE-KLGD 221

RESULT 13
US-11-012-762-10
; Sequence 10, Application US/11012762
; Publication No. US20050244815A1
; GENERAL INFORMATION:
; APPLICANT: Georgia State University Research Foundation, Inc.
; TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes
; FILE REFERENCE: GSUI.PCT
; CURRENT APPLICATION NUMBER: US/11/012,762
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US03/19300
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/390,046
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-762-10

Query Match 10.2%; Score 83; DB 7; Length 376;
Best Local Similarity 23.1%; Pred. No. 0.12;
Matches 42; Conservative 24; Mismatches 50; Indels 66; Gaps 8;

QY 3 GKLESKLSVIRN-----LNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKD 54
Db 68 GRSDADLVFLNLTSPEDQLNQGVLIKEIKQLCEVQHERRC----- 111

QY 55 SOPRGMAVTISVKCEKISXLSKSCENKIISFKEMNPPDNIKDTSKDI----- 100
Db 112 -----GVKFEVHLSRSPNSRALSFK-LSAPDLLKEVKFDVLPAYDLDLHLNLLK 160
QY 101 ----PFQ-----RSVPGHDKNQMFSSSYEGYFLACE--KERDLFKLI-----LKKEDEL 144
Db 161 PNQOQFYANLISGRTPPGKEGKLSICFMGLRKYFLNCRPTKLRLRLVTHWYQLCKE-KL 219

QY 145 GD 146
Db 220 GD 221

RESULT 14
US-11-012-762-16
; Sequence 16, Application US/11012762
; Publication No. US20050244815A1
; GENERAL INFORMATION:
; APPLICANT: Georgia State University Research Foundation, Inc.
; TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes
; FILE REFERENCE: GSUI.PCT
; CURRENT APPLICATION NUMBER: US/11/012,762
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US03/19300
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/390,046
; PRIOR FILING DATE: 2002-06-19
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Job time : 32 secs

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; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 16
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-762-16

Query Match      10.2%; Score 83; DB 7; Length 376;
Best Local Similarity 23.1%; Pred. No. 0.12;
Matches 42; Conservative 24; Mismatches 50; Indels 66; Gaps 8;

Qy      3 GKLESKLSVIRN-----LNDQVLFIDQGNRPLFEDMTSDCDNAPRTIFIISMVKD 54
Db      68 GRSDADLVVFLNNITSPEDQLNQOGLVLIKEIKQLCEVQHERRC-----111

Qy      55 SQPRGMATVISVCKEKISXLSCEKNIISFKEMNPPDNIKOTKSDII-----100
Db      112 -----GVKFEVHSLRSPNSRAISFK-LSAPDLLKEVKFDVLPAYDLLDHLNLIK 160

Qy      101 -----FFQ-----RSVPGHNDNMQFESSYEGYFLACE--KERDLFKLI-----LKKEDEL 144
Db      161 PNOQFYANLISGRTPPGKEGKLSICFMGLRKVFLNCRPTKLRLIRLVTHWYQLCKE-KL 219

Qy      145 GD 146
Db      220 GD 221

RESULT 15
US-11-012-762-40
; Sequence 40, Application US/11012762
; Publication No. US20050244815A1
; GENERAL INFORMATION:
; APPLICANT: Georgia State University Research Foundation, Inc.
; TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes
; FILE REFERENCE: GSUI.PCT
; CURRENT APPLICATION NUMBER: US/11/012,762
; PRIOR FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US03/19300
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/390,046
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 40
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-762-40

Query Match      10.2%; Score 83; DB 7; Length 376;
Best Local Similarity 23.1%; Pred. No. 0.12;
Matches 42; Conservative 24; Mismatches 50; Indels 66; Gaps 8;

Qy      3 GKLESKLSVIRN-----LNDQVLFIDQGNRPLFEDMTSDCDNAPRTIFIISMVKD 54
Db      68 GRSDADLVVFLNNITSPEDQLNQOGLVLIKEIKQLCEVQHERRC-----111

Qy      55 SQPRGMATVISVCKEKISXLSCEKNIISFKEMNPPDNIKOTKSDII-----100
Db      112 -----GVKFEVHSLRSPNSRAISFK-LSAPDLLKEVKFDVLPAYDLLDHLNLIK 160

Qy      101 -----FFQ-----RSVPGHNDNMQFESSYEGYFLACE--KERDLFKLI-----LKKEDEL 144
Db      161 PNOQFYANLISGRTPPGKEGKLSICFMGLRKVFLNCRPTKLRLIRLVTHWYQLCKE-KL 219

Qy      145 GD 146
Db      220 GD 221

Search completed: January 30, 2006, 08:52:39
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2006, 08:40:23 ; Search time 117 Seconds  
(without alignments)  
560.677 Million cell updates/sec

Title: US-09-716-356A-6  
Perfect score: 812  
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDELGDRSINFVTQVED 157

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA Main:\*

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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pcp.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pcp.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pcp.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pcp.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	811	99.9	157	3	US-09-775-046-9 Sequence 9, Appli
2	811	99.9	157	3	US-09-030-061-6 Sequence 6, Appli
3	811	99.9	157	4	US-10-100-057-6 Sequence 6, Appli
4	811	99.9	157	4	US-10-094-153-2 Sequence 2, Appli
5	811	99.9	157	4	US-10-260-576-4 Sequence 4, Appli
6	811	99.9	157	4	US-10-297-136-1 Sequence 1, Appli
7	811	99.9	157	4	US-10-311-491-3 Sequence 3, Appli
8	811	99.9	157	4	US-10-397-786A-3 Sequence 3, Appli
9	811	99.9	157	4	US-10-280-609-1 Sequence 1, Appli
10	811	99.9	157	4	US-10-648-308-14 Sequence 14, Appli
11	811	99.9	157	5	US-10-872-198-98 Sequence 98, Appli
12	811	99.9	157	5	US-10-823-964A-1 Sequence 1, Appli
13	811	99.9	157	5	US-10-666-490A-1 Sequence 1, Appli
14	811	99.9	157	5	US-10-518-333-1 Sequence 1, Appli
15	811	99.9	157	6	US-11-021-951-98 Sequence 98, Appli
16	811	99.9	158	4	US-10-693-195-7 Sequence 7, Appli
17	811	99.9	158	4	US-10-694-978-7 Sequence 7, Appli
18	811	99.9	193	3	US-09-798-075-1 Sequence 1, Appli
19	811	99.9	193	3	US-09-770-528-8 Sequence 8, Appli
20	811	99.9	193	4	US-10-311-491-1 Sequence 1, Appli
21	811	99.9	193	4	US-10-679-201-5 Sequence 5, Appli
22	811	99.9	193	5	US-10-706-869-1 Sequence 1, Appli
23	811	99.9	193	5	US-10-988-360-1 Sequence 1, Appli
24	811	99.9	203	4	US-10-823-964A-3 Sequence 3, Appli
25	811	99.9	233	4	US-10-311-491-10 Sequence 10, Appli
26	811	99.9	325	5	US-10-895-396-10 Sequence 10, Appli
27	811	99.9	361	5	US-10-895-396-8 Sequence 8, Appli

ALIGNMENTS

RESULT 1  
US-09-775-046-9  
; Sequence 9, Application US/09775046  
; Patent No. US20020102234A1  
; GENERAL INFORMATION:  
; APPLICANT: Debets, Johannes Eduard Maria Antonius  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Bazan, J. Fernando  
; APPLICANT: Kastelein, Robert A.  
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS  
; FILE REFERENCE: DX01073K  
; CURRENT APPLICATION NUMBER: US/09/775,046  
; CURRENT FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 60/179,638  
; PRIOR FILING DATE: 2000-02-02  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-775-046-9

Query Match 99.9%; Score 811; DB 3; Length 157;  
Best Local Similarity 99.4%; Pred. No. 2.3e-78;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
  
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQORSVPGHDKMKOFESSY 120  
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQORSVPGHDKMKOFESSY 120  
  
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157  
DB 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157

RESULT 2  
US-09-030-061-6  
; Sequence 6, Application US/09030061  
; Publication No. US20030095946A1  
; GENERAL INFORMATION:  
; APPLICANT: GILLISPIE, Matthew Todd  
; APPLICANT: HORWOOD, Nicole Joy  
; APPLICANT: UDAGAWA, No. US20030095946A1uyuki  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,061  
; FILING DATE: 25-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 55,468/1997

FILING DATE: 25-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: GILLISPIE-1  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-030-061-6

Query Match 99.9%; Score 811; DB 3; Length 157;  
Best Local Similarity 99.4%; Pred. No. 2.3e-78;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
  
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQORSVPGHDKMKOFESSY 120  
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQORSVPGHDKMKOFESSY 120  
  
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157  
DB 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157

RESULT 3  
US-10-100-057-6  
; Sequence 6, Application US/10100057  
; Publication No. US20020150555A1  
; GENERAL INFORMATION:  
; APPLICANT: GILLISPIE, Matthew Todd  
; APPLICANT: HORWOOD, Nicole Joy  
; APPLICANT: UDAGAWA, No. US20020150555A1uyuki  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/100,057  
; FILING DATE: 19-Mar-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,061  
; FILING DATE: 25-FEB-1998  
; APPLICATION NUMBER: JP 55,468/1997  
; FILING DATE: 25-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: GILLISPIE-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-100-057-6

Query Match          99.9%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.3e-78;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 1 YFGKLESKLSVIRNLNDQVLFDIDGGRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFDIDGGRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKOTKSDIIPFORSVPGHDNKMQFESSY 120
DB 61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKOTKSDIIPFORSVPGHDNKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 4
US-10-094-153-2
; Sequence 2, Application US/10094153
; Publication No. US20020169291A1
; GENERAL INFORMATION:
; APPLICANT: Dinarello, Charles
; APPLICANT: Kim, Soo Hyun
; TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
; FILE REFERENCE: 475
; CURRENT APPLICATION NUMBER: US/10/094,153
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/274,327
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-153-2

Query Match          99.9%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.3e-78;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 1 YFGKLESKLSVIRNLNDQVLFDIDGGRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFDIDGGRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKOTKSDIIPFORSVPGHDNKMQFESSY 120
DB 61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKOTKSDIIPFORSVPGHDNKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 5
US-10-260-576-4
; Sequence 4, Application US/10260576
; Publication No. US20030092130A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Koza
; APPLICANT: OKAMOTO, Iwao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:

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; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/208,869
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-297-136-1

Query Match          99.9%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.3e-78;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIDKTSDIIFQRSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIDKTSDIIFQRSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 7
US-10-311-491-3
; Sequence 3, Application US/10311491
; Publication No. US20030143198A1
; GENERAL INFORMATION:
; APPLICANT: Johanson, Kyung O.
; APPLICANT: Kirkpatrick, Robert B.
; APPLICANT: Shatzman, Allan R.
; APPLICANT: Ho, Yen Sen
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: Method for Preparing a Physiologically
; FILE REFERENCE: P51137
; CURRENT APPLICATION NUMBER: US/10/311,491
; CURRENT FILING DATE: 2002-12-16
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/211,832
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/224,128
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/264,923
; PRIOR FILING DATE: 2001-01-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-311-491-3

Query Match          99.9%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.3e-78;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIDKTSDIIFQRSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIDKTSDIIFQRSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
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DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 8
US-10-397-786A-3
; Sequence 3, Application US/10397786A
; Publication No. US20040018195A1
; GENERAL INFORMATION:
; APPLICANT: Griswold, Donald
; APPLICANT: Li, Li
; APPLICANT: Li, Jian
; TITLE OF INVENTION: DIABETES DISEASE DERIVED PROTEINS, COMPOSITIONS, METHODS AND USE
; FILE REFERENCE: CEN-0287
; CURRENT APPLICATION NUMBER: US/10/397,786A
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/367,902
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver 2.0
; SEQ ID NO 3
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-397-786A-3

Query Match          99.9%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.3e-78;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIDKTSDIIFQRSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIDKTSDIIFQRSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 9
US-10-280-609-1
; Sequence 1, Application US/10280609
; Publication No. US2004002336A1
; GENERAL INFORMATION:
; APPLICANT: Heavner, George
; APPLICANT: Snyder, Linda Anne
; APPLICANT: McCarthy, Stephen G.
; TITLE OF INVENTION: IL-18 OR MUT-IL-18R PROTEINS, ANTIBODIES, COMPOSITIONS,
; FILE REFERENCE: CEN0321
; CURRENT APPLICATION NUMBER: US/10/280,609
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/335,880
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-280-609-1

Query Match          99.9%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.3e-78;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
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QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQSVPGHDKMQFESSY 120  
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QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

## RESULT 10

US-10-646-308-14  
; Sequence 14, Application US/10646308  
; Publication No. US20040136992A1  
; GENERAL INFORMATION:  
; APPLICANT: BURTON, Paul B. J.  
; APPLICANT: DEISHER, Theresa A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE  
; FILE REFERENCE: 3432-B  
; CURRENT APPLICATION NUMBER: US/10/646,308  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: --to be assigned--  
; PRIOR FILING DATE: 2003-08-12  
; PRIOR APPLICATION NUMBER: 60/406,418  
; PRIOR FILING DATE: 2002-08-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 14  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-646-308-14

Query Match 99.9%; Score 811; DB 4; Length 157;  
Best Local Similarity 99.4%; Pred. No. 2.3e-78;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQSVPGHDKMQFESSY 120  
Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQSVPGHDKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

## RESULT 11

US-10-872-198-98  
; Sequence 98, Application US/10872198  
; Publication No. US2005002897A1  
; GENERAL INFORMATION:  
; APPLICANT: Ulrich HAUPTS  
; APPLICANT: Andre KOLTERMANN  
; APPLICANT: Andreas SCHERDIG  
; APPLICANT: Christian VOETSMERIER  
; APPLICANT: Ulrich Ketting  
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF  
; FILE REFERENCE: 04156.000204  
; CURRENT APPLICATION NUMBER: US/10/872,198  
; CURRENT FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 60/543,518  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/524,960  
; PRIOR FILING DATE: 2003-11-25  
; PRIOR APPLICATION NUMBER: EP 04003058  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: EP 03025871  
; PRIOR FILING DATE: 2003-11-11  
; PRIOR APPLICATION NUMBER: EP 03025851  
; PRIOR FILING DATE: 2003-11-10

; PRIOR APPLICATION NUMBER: EP 03013819  
; PRIOR FILING DATE: 2003-06-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 98  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-872-198-98

Query Match 99.9%; Score 811; DB 5; Length 157;  
Best Local Similarity 99.4%; Pred. No. 2.3e-78;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQSVPGHDKMQFESSY 120  
Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQSVPGHDKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

## RESULT 12

US-10-823-964A-1  
; Sequence 1, Application US/10823964A  
; Publication No. US20050008615A1  
; GENERAL INFORMATION:  
; APPLICANT: BAM, NARENDRA  
; APPLICANT: BONGERS, JACOB  
; APPLICANT: KIRKPATRICK, ROBERT B.  
; APPLICANT: JANSON, CHERYL A.  
; APPLICANT: JOHANSON, KYUNG  
; APPLICANT: QIU, XIANYANG  
; APPLICANT: YEH, PING  
; TITLE OF INVENTION: CONJUGATES COMPRISING HUMAN IL-18 AND  
; FILE REFERENCE: PU60053  
; CURRENT APPLICATION NUMBER: US/10/823,964A  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: 60/462,947  
; PRIOR FILING DATE: 2003-04-15  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-823-964A-1

Query Match 99.9%; Score 811; DB 5; Length 157;  
Best Local Similarity 99.4%; Pred. No. 2.3e-78;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQSVPGHDKMQFESSY 120  
Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQSVPGHDKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

## RESULT 13

US-10-666-490A-1



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; Sequence 1, Application US/10666490A
; Publication No. US2005006394A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jian;
; APPLICANT: Mbow, Lamine;
; APPLICANT: Goletz, Terry;
; APPLICANT: Peritt, David;
; TITLE OF INVENTION: METHOD OF INDUCING MATURATION OF DENDRITIC CELLS AND USES THEREOF
; FILE REFERENCE: CEN0312 NP
; CURRENT APPLICATION NUMBER: US/10/666,490A
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: 60/412,145
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver 3.0.
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-666-490A-1

Query Match          99.9%; Score 811; DB 5; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.3e-78;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTTIFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTTIFIISMVKDSQPRGM 60

QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQSVPGHNDKMQFESSY 120
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQSVPGHNDKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 14
US-10-518-333-1
; Sequence 1, Application US/10518333
; Publication No. US20050153880A1
; GENERAL INFORMATION:
; APPLICANT: Goto, Yukio
; APPLICANT: Kikkawa, Hideo
; APPLICANT: Kinoshita, Mine
; TITLE OF INVENTION: Method of Treating or Preventing IBD
; TITLE OF INVENTION: with IL-18
; FILE REFERENCE: TB00005
; CURRENT APPLICATION NUMBER: US/10/518,333
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/EP03/17744
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/392,176
; PRIOR FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-518-333-1

Query Match          99.9%; Score 811; DB 5; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.3e-78;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTTIFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTTIFIISMVKDSQPRGM 60

QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQSVPGHNDKMQFESSY 120
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQSVPGHNDKMQFESSY 120
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DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQSVPGHNDKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 15
US-11-021-951-98
; Sequence 98, Application US/11021951
; Publication No. US20050175581A1
; GENERAL INFORMATION:
; APPLICANT: HAUPTS, Ulrich
; APPLICANT: KOLTERMANN, Andre
; APPLICANT: SCHEIDIG, Andreas
; APPLICANT: VOTSMEIER, Christian
; APPLICANT: Ketting, Ulrich
; APPLICANT: COCO, Wayne Michael
; TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
; TITLE OF INVENTION: And Diagnostic Use Thereof
; FILE REFERENCE: 04156.0002U5
; CURRENT APPLICATION NUMBER: US/11/021,951
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 10/872,198
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 98
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-951-98

Query Match          99.9%; Score 811; DB 6; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.3e-78;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTTIFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTTIFIISMVKDSQPRGM 60

QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQSVPGHNDKMQFESSY 120
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQSVPGHNDKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

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Job time : 118 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2006, 08:33:47 : Search time 47 Seconds  
(without alignments)  
276.172 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDELGRSIMFTVQNEQ 157

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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5 COMB pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/6 COMB pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	811	99.9	157	2	US-09-700-609-1
3	811	99.9	157	2	US-09-775-046-9
4	811	99.9	157	2	US-10-100-057-6
5	811	99.9	157	2	US-09-398-412B-7
6	811	99.9	164	2	US-09-949-016-10506
7	811	99.9	193	1	US-09-949-016-6095
8	810	99.8	157	1	US-08-896-605A-6
9	810	99.8	157	1	US-08-896-501A-4
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12	810	99.8	157	2	US-08-558-818-1
13	810	99.8	157	2	US-08-974-469A-1
14	810	99.8	157	2	US-08-832-180-1
15	810	99.8	157	2	US-08-832-198-6
16	810	99.8	157	2	US-09-819-902-6
17	810	99.8	157	2	US-09-752-510-6
18	810	99.8	157	2	US-09-711-899-1
19	810	99.8	157	2	US-09-556-972-26
20	810	99.8	157	2	US-09-649-063-1
21	810	99.8	157	2	US-09-479-862-1
22	810	99.8	193	1	US-08-896-605A-2
23	810	99.8	193	1	US-08-896-501A-2
24	810	99.8	157	2	US-08-832-180-9
25	803	99.9	157	2	US-10-105-080-10
26	803	99.9	193	2	US-10-105-080-4
27	801	98.6	157	2	US-08-982-285-6
28	801	98.6	157	2	US-09-700-609-1
29	792	97.5	193	2	US-09-597-576-2
30	791	97.4	157	2	US-08-982-285-7
31	791	97.4	157	2	US-08-982-285-8
32	791	97.4	157	2	US-10-100-057-21
33	791	97.4	157	2	US-10-100-057-22
34	782	96.3	157	2	US-08-982-285-11
35	782	96.3	157	2	US-10-100-057-25
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37	781	96.2	157	2	US-10-100-057-23
38	772	95.1	157	2	US-08-982-285-12
39	772	95.1	157	2	US-10-100-057-26
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47	610	75.1	154	2	US-09-917-265A-5
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49	517	63.7	157	2	US-10-100-057-27
50	515	63.4	157	2	US-08-982-285-5
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52	515	63.4	157	2	US-10-105-080-11
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54	515	63.4	157	2	US-10-100-057-7
55	515	63.4	158	2	US-09-398-412B-8
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59	513	63.2	157	2	US-08-558-818-7
60	513	63.2	157	2	US-08-974-469A-7
61	513	63.2	157	2	US-08-832-180-8
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67	513	63.2	157	2	US-09-711-899-7
68	513	63.2	157	2	US-09-556-972-27
69	513	63.2	157	2	US-09-649-063-2
70	511	62.9	192	2	US-10-105-080-5
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73	359	44.2	133	2	US-09-917-265A-2
74	259	31.9	50	2	US-08-832-198-2
75	259	31.9	50	2	US-09-819-902-2
76	259	31.9	50	2	US-09-752-510-2
77	96	11.8	25	2	US-08-558-818-4
78	96	11.8	25	2	US-08-974-469A-4
79	96	11.8	25	2	US-08-832-180-4
80	96	11.8	25	2	US-08-832-198-8
81	96	11.8	25	2	US-09-819-902-8
82	96	11.8	25	2	US-09-752-510-8
83	96	11.8	25	2	US-09-711-899-4
84	90	11.1	17	2	US-08-832-198-5
85	90	11.1	17	2	US-09-819-902-5
86	90	11.1	17	2	US-09-752-510-5
87	90	11.1	17	2	US-10-100-057-13
88	85	10.5	333	2	US-09-270-767-31995
89	85	10.5	333	2	US-09-270-767-47212
90	83	10.2	697	2	US-09-248-796A-26663
91	81	10.0	155	6	US-09-248-796A-26663
92	81	10.0	267	6	5494663-5
93	78.5	9.7	363	2	US-09-248-796A-19880
94	77	9.5	243	2	US-09-248-796A-20638
95	76.5	9.4	270	1	US-08-611-880-1
96	76.5	9.4	270	2	US-09-085-305-13
97	75.5	9.3	270	2	US-09-085-305-20
98	75	9.2	267	2	US-09-134-001C-3520
99	75	9.2	637	2	US-09-248-796A-19134
100	74.5	9.2	467	2	US-09-522-775A-2

ALIGNMENTS

RESULT 1  
US-08-982-285-4  
; Sequence 4, Application US/08982285  
; Patent No. 6476197  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, Kojo  
; APPLICANT: OKAMOTO, Iwao  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: POLYPEPTIDES  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 7th Street N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/982,285  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 333,037/96  
; FILING DATE: NO. 6476197ember 29, 1996  
; APPLICATION NUMBER: JP 20,906/97  
; FILING DATE: January 21, 1997  
; APPLICATION NUMBER: JP 10,053,503  
; FILING DATE: NO. 6476197ember 14, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: YAMAMOTO=15  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-982-285-4

Query Match 99.9%; Score 811; DB 2; Length 157;  
Best Local Similarity 99.4%; Pred. No. 4.7e-88;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFFORSVPGHDNKMQFESSY 120  
Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTSKDIIFFORSVPGHDNKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 2  
US-09-700-609-1  
; Sequence 1, Application US/09700609  
; Patent No. 6582689

; GENERAL INFORMATION:  
; APPLICANT: Johnson, Randall K  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: P50777  
; CURRENT APPLICATION NUMBER: US/09/700,609  
; CURRENT FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/086,560  
; PRIOR FILING DATE: 1999-05-21  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Human  
US-09-700-609-1  
Query Match 99.9%; Score 811; DB 2; Length 157;  
Best Local Similarity 99.4%; Pred. No. 4.7e-88;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFFORSVPGHDNKMQFESSY 120  
Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTSKDIIFFORSVPGHDNKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 3  
US-09-775-046-9  
; Sequence 9, Application US/09775046  
; Patent No. 6843987  
; GENERAL INFORMATION:  
; APPLICANT: Debets, Johannes Eduard Maria Antonius  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Bazan, J. Fernando  
; APPLICANT: Kastelein, Robert A.  
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS  
; FILE REFERENCE: DX01073K  
; CURRENT APPLICATION NUMBER: US/09/775,046  
; CURRENT FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 60/179,638  
; PRIOR FILING DATE: 2000-02-02  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-775-046-9

Query Match 99.9%; Score 811; DB 2; Length 157;  
Best Local Similarity 99.4%; Pred. No. 4.7e-88;  
Matches 156; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFFORSVPGHDNKMQFESSY 120  
Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTSKDIIFFORSVPGHDNKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

## RESULT 4

US-10-100-057-6  
; Sequence 6, Application US/10100057  
; Patent No. 6896880  
; GENERAL INFORMATION:  
; APPLICANT: GILLISPIE, Matthew Todd  
; HORMWOOD, Nicole Joy  
; UDAGAWA, No. 6896880yuyuki  
; KURIMOTO, Masashi  
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/100,057  
; FILING DATE: 19-Mar-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,061  
; FILING DATE: 25-FEB-1998  
; APPLICATION NUMBER: JP 55,468/1997  
; FILING DATE: 25-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: GILLISPIE=1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-100-057-6

Query Match 99.9%; Score 811; DB 2; Length 157;  
Best Local Similarity 99.4%; Pred. No. 4.7e-88;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESY 120  
Db 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESY 120  
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

## RESULT 5

US-09-398-412B-7  
; Sequence 7, Application US/09398412B  
; Patent No. 6680380  
; GENERAL INFORMATION:  
; APPLICANT: Timans, Jacqueline C.  
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reage  
; FILE REFERENCE: DX0904K

; CURRENT APPLICATION NUMBER: US/09/398,412B  
; CURRENT FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: US 60/100948  
; PRIOR FILING DATE: 1998-09-18  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 158  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-398-412B-7

Query Match 99.9%; Score 811; DB 2; Length 158;

Best Local Similarity 99.4%; Pred. No. 4.7e-88;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
Db 2 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 61  
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESY 120  
Db 62 AVTISVKCEKISLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESY 121  
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157  
Db 122 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 158

## RESULT 6

US-09-949-016-10506  
; Sequence 10506, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10506  
; LENGTH: 164  
; TYPE: PRT  
; ORGANISM: Human  
; US-09-949-016-10506

Query Match 99.9%; Score 811; DB 2; Length 164;  
Best Local Similarity 99.4%; Pred. No. 5e-88;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
Db 8 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 67  
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESY 120  
Db 68 AVTISVKCEKISLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESY 127  
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157  
Db 128 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 164

## RESULT 7

US-09-949-016-6095

```
; Sequence 6095, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6095
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6095

Query Match          99.9%; Score 811; DB 2; Length 193;
Best Local Similarity 99.4%; Pred. No. 6.2e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 96
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKTKSDIIFQRSVPGHDKMKQFESSY 120
DB 97 AVTISVKCEKISTLSCEKNIISFKEMNPPDNIKTKSDIIFQRSVPGHDKMKQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 8
US-08-896-605A-6
; Sequence 6, Application US/08896605A
; Patent No. 5879942
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,605A
; FILING DATE: 18 JULY 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207,691/1996
; FILING DATE: 19-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 156,062/1997
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618

; Sequence 6095, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6095
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6095

Query Match          99.9%; Score 811; DB 2; Length 193;
Best Local Similarity 99.4%; Pred. No. 6.2e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 96
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKTKSDIIFQRSVPGHDKMKQFESSY 120
DB 97 AVTISVKCEKISTLSCEKNIISFKEMNPPDNIKTKSDIIFQRSVPGHDKMKQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 9
US-08-896-501A-4
; Sequence 4, Application US/08896501A
; Patent No. 5891663
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,501A
; FILING DATE: 18-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 213,267/1996
; FILING DATE: 25-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 31,474/1997
; FILING DATE: 31-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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MOLECULE TYPE: peptide
US-08-896-501A-4

Query Match          99.8%; Score 810; DB 1; Length 157;
Best Local Similarity 100.0%; Pred. No. 6.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQFORSVPGHNDKMQFESSY 120
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQFORSVPGHNDKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 10
US-08-884-324-1
; Sequence 1, Application US/08884324
; Patent No. 6060283
; GENERAL INFORMATION:
; APPLICANT: Takatori OKURA
; APPLICANT: Kakuji TORIOGE
; APPLICANT: Masahi KURIMOTO
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
; OF INDUCING THE PRODUCTION OF INTERFERON-
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; PRIOR APPLICATION NUMBER: US/08/884,324
; CLASSIFICATION: 435
; APPLICATION DATA:
; FILING DATE: 27-JUN-1996
; APPLICATION NUMBER: JP 185,305/96
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: OKURA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-884-324-1

Query Match          99.8%; Score 810; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 6.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQFORSVPGHNDKMQFESSY 120
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQFORSVPGHNDKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 11
US-08-996-338-26
; Sequence 26, Application US/08996338
; Patent No. 6087116
; GENERAL INFORMATION:
; APPLICANT: TORIOGE, Kakuji
; APPLICANT: OKURA, Takatori
; APPLICANT: KURIMOTO, Masahi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,338
; FILING DATE: 22-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 74,697/1997
; FILING DATE: 12-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 215,488/1997
; FILING DATE: 28-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 291,837/1997
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIOGE-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-996-338-26

Query Match          99.8%; Score 810; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 6.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQFORSVPGHNDKMQFESSY 120
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQFORSVPGHNDKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
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RESULT 12

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US-08-558-818-1
/ Sequence 1, Application US/08558818
/ Patent No. 6197297
/ GENERAL INFORMATION:
/
/ APPLICANT:
/
/ APPLICANT: NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
/
/ APPLICANT: KENKYUJO
/
/ APPLICANT: KUNIKATA, Toshio
/
/ APPLICANT: TANIGUCHI, Mutsuko
/
/ APPLICANT: KOHNO, Keizo
/
/ APPLICANT: KURIMOTO, Masashi
/
/ TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
/
/ TITLE OF INVENTION: WHICH INDUCES INTERFERON- PRODUCTION
/
/ NUMBER OF SEQUENCES: 9
/
/ CORRESPONDENCE ADDRESS:
/
/ ADDRESSEE: Browdy and Neimark
/
/ STREET: 419 Seventh Street N.W. Ste. 300
/
/ CITY: Washington
/
/ STATE: D.C.
/
/ COUNTRY: USA
/
/ ZIP: 20004
/
/ COMPUTER READABLE FORM:
/
/ MEDIUM TYPE: Floppy disk
/
/ COMPUTER: IBM PC compatible
/
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/
/ SOFTWARE: Word Perfect Version 5.0
/
/ ATTORNEY/AGENT INFORMATION:
/
/ NAME: Browdy, Roger L.
/
/ REGISTRATION NUMBER: 25,618
/
/ REFERENCE/DOCKET NUMBER: FELICI-1
/
/ TELECOMMUNICATION INFORMATION:
/
/ TELEPHONE: (202) 628-5197
/
/ TELEFAX: (202) 737-3528
/
/ CURRENT APPLICATION DATA:
/
/ APPLICATION NUMBER: US/08/558,818
/
/ FILING DATE:
/
/ CLASSIFICATION: 530
/
/ PRIOR APPLICATION DATA:
/
/ PRIOR APPLICATION DATA: JP 58,240/95
/
/ PRIOR APPLICATION DATA: February 23, 1995
/
/ INFORMATION FOR SEQ ID NO: 1:
/
/ SEQUENCE CHARACTERISTICS:
/
/ LENGTH: 157 amino acids
/
/ TYPE: amino acid
/
/ TOPOLOGY: linear
/
/ MOLECULE TYPE: peptide
/
/ US-08-558-818-1

```

APPLICANT: OKAMURA, Haruki  
APPLICANT: KURIMOTO, Masashi  
TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING  
TITLE OF INVENTION: POLYPEPTIDE  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street N.W. Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect Version 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/832,180  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/558,191  
FILING DATE:  
APPLICATION NUMBER: JP 304,203/94  
FILING DATE: No. 6214584ember 15, 1994  
APPLICATION NUMBER: 10048102  
FILING DATE: September 18, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Browdy, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: USHIO-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-832-180-1

Query Match 99.8%; Score 810; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 6.2e-88;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISXLSCKENKIIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMQFESSY 120  
Db 61 AVTISVKCEKISXLSCKENKIIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMQFESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 15  
US-08-832-198-6  
Sequence 6, Application US/08032198  
Patent No. 6242255  
GENERAL INFORMATION:  
APPLICANT: AKITA, Kenji  
APPLICANT: NUKADA, Yoshiyuki  
APPLICANT: FUJII, Mitsuhiro  
APPLICANT: TANIMOTO, Tadao  
APPLICANT: KURIMOTO, Masashi  
TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA  
TITLE OF INVENTION: PRODUCTION BY IMMUNOCOMPETENT CELL

NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
STREET: 419 Seventh Street N.W., Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/832,198  
FILING DATE: 08-APR-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/721,018  
FILING DATE: 25-SEP-1996  
APPLICATION NUMBER: JP 95-270725  
FILING DATE: 26-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 96-067434  
FILING DATE: 29-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP not yet received  
FILING DATE: 20-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: AKITA-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: "Xaa" in position 73 is either  
OTHER INFORMATION: 'Ile' or 'Thr'  
US-08-832-198-6

Query Match 99.8%; Score 810; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 6.2e-88;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISXLSCKENKIIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMQFESSY 120  
Db 61 AVTISVKCEKISXLSCKENKIIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMQFESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

Search completed: January 30, 2006, 08:41:58  
Job time : 48 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2006, 08:19:16 ; Search time 134 Seconds  
(without alignments)  
514.795 Million cell updates/sec

US-09-716-356A-6

Title: Perfect score: 812

Sequence: 1 YFGKLESKLSVRLNDQVL.....LKKEDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A Geneseq 21:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	811	99.9	157	2	Aaw77077 Human int
2	811	99.9	157	3	Aay57570 Human int
3	811	99.9	157	4	Aag65351 Human int
4	811	99.9	157	4	Aag65294 Human int
5	811	99.9	157	4	Aae06661 Human int
6	811	99.9	157	5	AB04389 Human IL-
7	811	99.9	157	5	AAE17134 Human IL-
8	811	99.9	157	5	AAE16954 Human act
9	811	99.9	157	6	ABG73359 Human int
10	811	99.9	157	6	ADA50616 Human mat
11	811	99.9	157	6	ADA50610 Human mat
12	811	99.9	157	6	ABR83372 Human int
13	811	99.9	157	7	ADE06775 Human int
14	811	99.9	157	8	ADH54826 Human int
15	811	99.9	157	8	ADL24279 Human IL-
16	811	99.9	157	8	ADN35070 Human IL-
17	811	99.9	157	8	ADG73677 Human int
18	811	99.9	157	8	ADU06893 Human int
19	811	99.9	157	8	ADU49842 Human int
20	811	99.9	157	9	ADV900268 Human int
21	811	99.9	157	9	ADY86605 Human rec
22	811	99.9	157	9	ADZ77759 Human int
23	811	99.9	157	9	ADZ77756 Human int
24	811	99.9	157	9	AEB93714 Human mut

25	811	99.9	157	9	ABE93702	Human wil
26	811	99.9	158	3	AAY85167	Human int
27	811	99.9	158	8	ADJ88309	Human int
28	811	99.9	158	8	ADO04682	Human int
29	811	99.9	177	6	ADA50614	Mature co
30	811	99.9	180	2	AAW48959	Wild-type
31	811	99.9	193	2	AAW22047	Interfero
32	811	99.9	193	2	AAW46592	Amino aci
33	811	99.9	193	4	AAAB30541	A human I
34	811	99.9	193	4	AAAG63830	Amino aci
35	811	99.9	193	5	AAE16953	Human pre
36	811	99.9	193	8	ADN41835	Amino aci
37	811	99.9	193	8	ADP12432	Protein e
38	811	99.9	193	8	ADP64786	Human int
39	811	99.9	193	9	ADZ51271	Amino aci
40	811	99.9	193	9	ADZ70835	Human int
41	811	99.9	193	9	ABE28907	Human int
42	811	99.9	203	8	ADU06895	Human int
43	811	99.9	233	5	AAE16959	Ubiquitin
44	811	99.9	325	9	ADY22167	Human IL-
45	811	99.9	361	9	ADY22165	Human IL-
46	811	99.9	536	5	AAE16957	Human pro
47	811	99.9	588	5	AAE16958	Human pro
48	811	99.9	1048	5	AAE16960	Ubiquitin
49	810	99.8	157	2	AAE99564	Human int
50	810	99.8	157	2	AAE99558	Human mat
51	810	99.8	157	2	AAW15701	Interfero
52	810	99.8	157	2	AAW24258	Human pro
53	810	99.8	157	2	AAW63810	Human IL-
54	810	99.8	157	2	AAW52176	Interfero
55	810	99.8	157	2	AAW77158	Human int
56	810	99.8	157	2	AAW37741	IFN-gamma
57	810	99.8	157	2	AAI39799	Interleuk
58	810	99.8	157	3	AAI53904	Sequence
59	810	99.8	157	3	AAI44597	Human int
60	810	99.8	157	4	AAE82408	Human int
61	810	99.8	157	6	ABR83405	Human int
62	810	99.8	157	6	ABR83406	Human int
63	810	99.8	157	6	ABR83399	Human int
64	810	99.8	157	6	ABR83395	Human int
65	810	99.8	193	2	AAE99560	Human int
66	810	99.8	193	2	AAW52172	Interfero
67	810	99.8	193	2	AAW47429	Interfero
68	810	99.8	193	2	AAW37740	Interfero
69	810	99.8	193	3	AAI53908	Amino aci
70	810	99.8	193	4	AAE82409	Human int
71	810	99.8	193	8	ADL24278	Human IL-
72	809	99.6	157	6	ABR83403	Human int
73	808	99.5	157	6	ABR83407	Human int
74	808	99.5	157	6	ABR83404	Human int
75	808	99.5	157	6	ABR83402	Human int
76	808	99.5	157	6	ABR83400	Human int
77	808	99.5	157	6	ABR83401	Human int
78	808	99.5	157	6	ABR83394	Human int
79	808	99.5	157	6	ABR83397	Human int
80	808	99.5	157	6	AAW77082	Interleuk
81	807	99.4	193	6	ABG73367	Human mat
82	807	99.4	157	6	ABR83396	Human int
83	807	99.4	157	6	ABR83398	Human int
84	807	99.4	193	6	ABG73366	Human pre
85	805	99.1	157	6	ABG73364	Human mat
86	805	99.1	157	6	ABG73363	Human mat
87	805	99.1	157	6	ABR83408	Human int
88	805	99.1	157	6	ADU49654	Human IL-
89	805	99.1	193	6	ABG73360	Human pre
90	805	99.1	193	6	ABG73361	Human pre
91	805	99.1	325	9	ADY22168	Human IL-
92	805	99.1	361	9	ADY22166	Human IL-
93	803	98.9	157	7	AAE39507	Human mat
94	803	98.9	157	8	ADU49656	Human IL-
95	803	98.9	193	2	AAW31757	Interfero
96	803	98.9	193	7	AAE39505	Human int
97	801	98.6	157	2	AAW77083	Human int

98 801 98.6 157 2 AAW48961 Aaw48961 Mutant hu  
99 801 98.6 157 8 ADU06896 Adu06896 Human int  
100 801 98.6 181 3 AAB23797 Aab23797 Human int

ALIGNMENTS

RESULT 1  
AAW77077  
ID AAW77077 standard; peptide; 157 AA.  
XX  
AC AAW77077;  
XX  
DT 16-NOV-1998 (first entry)  
XX  
DE Human interleukin 18.  
XX  
DE Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;  
KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;  
KW chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.  
XX  
OS Homo sapiens.  
XX  
PN EP861663-A2.  
XX  
PD 02-SEP-1998.  
XX  
PF 24-FEB-1998; 98EP-00301352.  
XX  
PR 25-FEB-1997; 97JP-00055468.  
XX  
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
XX  
PI Gillespie MT, Horwood NJ, Udagawa N, Kurimoto M;  
XX WPI; 1998-448964/39.  
DR N-PSDB; AAW48226.  
XX  
PT Use of interleukin-18 to inhibit osteoclast formation - in treatment of  
e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome, osteosarcoma,  
PT chronic rheumatoid arthritis, deformity ostitis, primary hyperthyroidism  
and osteoporosis.  
XX  
PS Claim 4; Page 18; 56pp; English.

XX Interleukin-18 (IL-18) or a functional equivalent can be used for  
inhibition of osteoclast formation. IL-18 is used for treating or  
preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma  
Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid  
arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and  
osteoporosis  
XX  
SQ Sequence 157 AA;  
Query Match 99.9%; Score 811; DB 2; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPGHDKMKQFESSY 120  
DB 61 AVTISVKCEKISTLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPGHDKMKQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
RESULT 2

AAW57570  
ID AAW57570 standard; protein; 157 AA.  
XX  
AC AAW57570;  
XX  
DT 06-MAR-2000 (first entry)  
XX  
DE Human interleukin 18 protein sequence SEQ ID NO:1.  
XX  
KW Human; interleukin 18; IL-18; potentiator; IGF; tumour; cancer;  
KW interferon-gamma-inducing factor; growth inhibition; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO9959565-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 20-MAY-1999; 99WO-US011160.  
XX  
PR 21-MAY-1998; 98US-0086560P.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
PI Johnson RK;  
XX  
DR WPI; 2000-062368/05.  
XX  
PT New polypeptides, useful for preparation of composition for preventing  
and/or treating cancer by inhibiting tumor growth.  
XX  
PS Claim 1; Page 49-50; 53pp; English.

XX The present sequence represents human interleukin 18 (IL-18). The present  
invention describes a compound comprising human or murine IL-18 in  
combination with a chemotherapeutic agent (I). Also described are: (1) a  
method of preventing and/or treating cancer in a mammal comprising the  
administration of a cancer inhibiting amount of (I) comprising the IL-18  
protein and the chemotherapeutic agent and optionally a pharmaceutically  
acceptable carrier; and (2) a method of inhibiting the growth of tumour  
cells in a mammal sensitive to a composition comprising human IL-18  
and/or murine IL-18 and the chemotherapeutic agent (and optionally a  
pharmaceutically acceptable carrier), comprising administering to a  
mammal afflicted with the tumour cells an effective tumour cell growth  
inhibiting amount of (I). The IL-18 protein in conjunction with a  
chemotherapeutic agent is useful in a method for preventing and/or  
treating cancer in mammals by inhibiting the growth of tumours or  
cancerous cells in mammals  
XX  
SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 3; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPGHDKMKQFESSY 120  
DB 61 AVTISVKCEKISTLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPGHDKMKQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
RESULT 3  
AAG65351  
ID AAG65351 standard; protein; 157 AA.  
XX  
AC AAG65351;

```
XX 30-NOV-2001 (first entry)
XX DT
XX DE Human interleukin-18 (IL-18) protein fragment.
XX IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
XX KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
XX KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.
XX OS Homo sapiens.
XX PN WO200158956-A2.
XX PD 16-AUG-2001.
XX PF 09-FEB-2001; 2001WO-US004170.
XX PR 10-FEB-2000; 2000US-0181608P.
XX PA (BADI ) BASF AG.
XX PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
XX PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
XX PI Lennard SN;
XX DR WPI; 2001-550020/61.
XX Novel antibodies and compounds capable of binding to human interleukin-18
XX useful for treating, e.g., inflammatory disorders, neurological
XX disorders, heart failure, myocardial infarction, and autoimmune diseases.
XX Disclosure; Page 14; 91pp; English.
XX PS The invention provides isolated antibodies, or antigen-binding portions,
XX CC that are capable of binding to human interleukin-18 (IL-18). The
XX CC antibodies may be used to inhibit human IL-18 activity in, and treat a
XX CC disorder where IL-18 is detrimental in, a human subject suffering from,
XX CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
XX CC inflammatory bowel disease, and osteoarthritis), neurological disorders
XX CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
XX CC stroke), heart failure, myocardial infarction, autoimmune diseases such
XX CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
XX CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
XX CC antibody may occur before, concurrent, or after administration of a
XX CC second agent selected from an antibody, or fragment, capable of binding
XX CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
XX CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
XX CC agents. The present sequence represents a human IL-18 protein fragment
XX SQ Sequence 157 AA;
Query Match 99.9%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 1:5e-82;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKQSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKQSQPRGM 60
Qy 61 AVTISVCKEKSXLSCENKIIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDNKMOPESSY 120
Db 61 AVTISVCKEKSXLSCENKIIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDNKMOPESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
RESULT 4
AAG65294
ID AAG65294 standard; protein; 157 AA.
XX AC AAG65294;
```

```
XX 30-NOV-2001 (first entry)
XX DT
XX DE Human interleukin-18 (IL-18) protein fragment.
XX IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
XX KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
XX KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.
XX OS Homo sapiens.
XX PN WO200158956-A2.
XX PD 16-AUG-2001.
XX PF 09-FEB-2001; 2001WO-US004170.
XX PR 10-FEB-2000; 2000US-0181608P.
XX PA (BADI ) BASF AG.
XX PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
XX PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
XX PI Lennard SN;
XX DR WPI; 2001-550020/61.
XX Novel antibodies and compounds capable of binding to human interleukin-18
XX useful for treating, e.g., inflammatory disorders, neurological
XX disorders, heart failure, myocardial infarction, and autoimmune diseases.
XX Disclosure; Page 14; 91pp; English.
XX PS The invention provides isolated antibodies, or antigen-binding portions,
XX CC that are capable of binding to human interleukin-18 (IL-18). The
XX CC antibodies may be used to inhibit human IL-18 activity in, and treat a
XX CC disorder where IL-18 is detrimental in, a human subject suffering from,
XX CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
XX CC inflammatory bowel disease, and osteoarthritis), neurological disorders
XX CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
XX CC stroke), heart failure, myocardial infarction, autoimmune diseases such
XX CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
XX CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
XX CC antibody may occur before, concurrent, or after administration of a
XX CC second agent selected from an antibody, or fragment, capable of binding
XX CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
XX CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
XX CC agents. The present sequence represents a human IL-18 protein fragment
XX SQ Sequence 157 AA;
Query Match 99.9%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 1:5e-82;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKQSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKQSQPRGM 60
Qy 61 AVTISVCKEKSXLSCENKIIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDNKMOPESSY 120
Db 61 AVTISVCKEKSXLSCENKIIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDNKMOPESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
RESULT 4
AAG65294
ID AAG65294 standard; protein; 157 AA.
XX AC AAG65294;
```

XX 16-OCT-2001 (first entry)  
XX Human interleukin-1gamma (IL-1gamma) protein.  
XX Human; interleukin-1gamma; IL-1gamma; virucide; hepatotropic; fever;  
XX immunological disorder; tumour; inflammatory disorder; hypoglycaemia;  
KW autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;  
KW psoriasis; viral infection; allergy; cytokine; HIV; drug screening.  
XX  
OS Homo sapiens.  
XX WO200157219-A2.  
XX  
XX 09-AUG-2001.  
XX  
XX 01-FEB-2001; 2001WO-US003285.  
XX  
XX 02-FEB-2000; 2000US-0179638P.  
XX  
XX (SCHE ) SCHERING CORP.  
XX  
XX Debets JEMA, Timans JC, Bazan JF, Kastelein RA;  
XX WPI; 2001-488886/53.  
XX  
XX Novel isolated or recombinant antigenic interleukin-1 delta or epsilon  
XX polypeptide useful for treating conditions exhibiting abnormal expression  
XX of interleukin such as immunological disorders, tumor and allergy.  
XX  
XX Disclosure; Fig 1; 103pp; English.  
XX  
XX The invention relates to recombinant antigenic interleukin-1 like  
XX molecules and their corresponding nucleic acid sequences, designated as  
XX interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon). IL  
XX -1delta and IL-1epsilon are useful for treating conditions exhibiting  
XX abnormal expression of the interleukin such as immunological disorders,  
XX tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,  
XX allergy, autoimmune diseases and infectious diseases (e.g., pulmonary  
XX tuberculosis, leprosy, fulminant hepatitis, and viral infections such as  
XX HIV). The invention also relates to methods of using the composition  
XX containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic  
XX utilities. IL-1delta is used as an immunogen for the production of  
XX antisera or antibodies specific, e.g., capable of distinguishing between  
XX IL-1 family members and an IL-1delta, for the interleukin or its  
XX fragment. The purified interleukin is used as a reagent to detect any  
XX antibodies generated in response to the presence of elevated levels of  
XX expression, or immunological disorders which lead to antibody production  
XX to the endogenous cytokine. The invention also contemplates the use of  
XX competitive drug screening assays. The present sequence is human  
XX interleukin-1gamma (IL-1gamma) protein related to the invention  
XX  
SQ Sequence 157 AA;  
  
Query Match 99.9%; Score 811; DB 4; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMVKDSQPRGM 60  
  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFORSVPGHDNKNQFESSY 120  
DB 61 AVTISVKCEKISTLSCEKNIISFKEMNPPDNIKDTSIIFFORSVPGHDNKNQFESSY 120  
  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
  
RESULT 6  
ABB04389  
Query Match 99.9%; Score 811; DB 4; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMVKDSQPRGM 60  
  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFORSVPGHDNKNQFESSY 120  
DB 61 AVTISVKCEKISTLSCEKNIISFKEMNPPDNIKDTSIIFFORSVPGHDNKNQFESSY 120  
  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
  
RESULT 6  
ABB04389

ID ABB04389 standard; protein; 157 AA.  
XX  
AC ABB04389;  
XX  
DT 21-MAY-2002 (first entry)  
XX  
DE Human IL-18.  
XX  
KW Human; IL-18; interleukin-18; cancer.  
XX  
OS Homo sapiens.  
XX  
PN CN1326992-A.  
XX  
PD 19-DEC-2001.  
XX  
PF 07-JUN-2000; 2000CN-00107993.  
XX  
PR 07-JUN-2000; 2000CN-00107993.  
XX  
PA (SHUA-) SHUANGLU PHARM CO LTD BEIJING.  
XX  
PI Xu M, Wang Y, Huang X;  
XX  
DR WPI; 2002-217571/28.  
DR N-PSDB; ABL41315.  
XX  
XX Gene cloning, product preparation and use of Chinese interleukin-18  
XX subype (53 Arg IL-18), useful for treating of cancer and other disease.  
XX  
PS Claim 1; Page 7 (Disclosure); 8pp; Chinese.  
XX  
XX The invention relates to the preparation of recombinant human interleukin  
XX -18 for treating of cancer and other disease  
XX  
SQ Sequence 157 AA;  
  
Query Match 99.9%; Score 811; DB 5; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMVKDSQPRGM 60  
  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFORSVPGHDNKNQFESSY 120  
DB 61 AVTISVKCEKISTLSCEKNIISFKEMNPPDNIKDTSIIFFORSVPGHDNKNQFESSY 120  
  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
  
RESULT 7  
AAE17134  
ID AAE17134 standard; protein; 157 AA.  
XX  
AC AAE17134;  
XX  
DT 22-APR-2002 (first entry)  
XX  
DE Human IL-18 protein.  
XX  
KW Human; viral disease; IL-18; interferon-gamma-inducing factor; IGIF; HSV;  
KW influenza virus; human immunodeficiency virus; HIV; herpes simplex virus;  
KW hepatitis A virus; HAV; hepatitis B virus; HBV; human papillomavirus;  
KW HPV; hepatitis C virus; HCV.  
XX  
OS Homo sapiens.  
XX  
PN WO200193898-A1.  
XX

PD 13-DEC-2001.  
 XX  
 PF 01-JUN-2001; 2001WO-US017924.  
 XX  
 PR 02-JUN-2000; 2000US-0208869P.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Esser KM, Rosenberg M, Tal-Singer R, Woodnutt G, Chisari FV;  
 XX  
 DR WPI; 2002-154554/20.  
 XX  
 XX Treatment of disease caused by e.g. influenza virus comprises  
 PT administration of composition containing polypeptide, having identity of  
 PT amino acid sequences.  
 XX  
 XX Claim 1; Fig 1; 41pp; English.  
 PS  
 XX The invention relates to a method for treating viral diseases with IL-18,  
 CC also known as interferon-gamma-inducing factor (IGIF) and IL-18  
 CC combinations. The method involves administering a composition comprising  
 CC IL-18 and IL-18 in combination with other agents. The method is used for  
 CC treating diseases caused by viruses such as influenza virus, human  
 CC immunodeficiency virus (HIV), herpes simplex virus (HSV), hepatitis A  
 CC virus (HAV), hepatitis B virus (HBV), human papillomavirus (HPV) and  
 CC hepatitis C virus (HCV). The present sequence is human IL-18 protein  
 XX  
 SQ Sequence 157 AA;  
  
 Query Match 99.9%; Score 811; DB 5; Length 157;  
 Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
 DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
  
 QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSKSDIIFQSVPGHDNKMQFESSY 120  
 DB 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTSKSDIIFQSVPGHDNKMQFESSY 120  
  
 QY 121 EGYFLACEKERDLFKILKKEDELGDRSIMFTVQNE 157  
 DB 121 EGYFLACEKERDLFKILKKEDELGDRSIMFTVQNE 157  
  
 RESULT 8  
 AAEL6954  
 ID AAEL6954 standard; protein; 157 AA.  
 XX  
 AC AAEL6954;  
 XX  
 DT 18-APR-2002 (first entry)  
 XX  
 DE Human active interleukin-18 (IL-18) protein.  
 XX  
 KW Human; interleukin-18; IL-18; caspase; interferon gamma; IFN-gamma;  
 KW immunocompetent.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200198455-A2.  
 XX  
 PD 27-DEC-2001.  
 XX  
 XX 11-JUN-2001; 2001WO-US018804.  
 XX  
 PF 15-JUN-2000; 2000US-0211832P.  
 PR 10-AUG-2000; 2000US-0224128P.  
 PR 20-JAN-2001; 2001US-0264923P.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Dinarello C, Kim SH;  
  
 JOHANSON KO, Kirkpatrick RB, Shatzman AR, Hoy YS, McDevitt P;  
 WPI; 2002-139786/18.  
 Activation of precursor polypeptide e.g. interleukin-18 polypeptide  
 useful for inducing interferon-gamma production, comprises contacting or  
 co-expressing caspase 4 or caspase 5 with precursor polypeptide.  
 Claim 9; Fig 3; 64pp; English.  
 The invention relates to a method for the in vitro activation of human  
 precursor interleukin-18 (Pro-IL-18) with an activating enzyme. The  
 method comprises contacting precursor IL-18 with 5 are members of a family  
 of cysteine proteases that include interleukin-beta converting enzyme  
 (ICE), which preferentially cleave substrates containing a protease  
 activation motif. The methods are useful for producing physiologically  
 active polypeptide e.g. active IL-18 polypeptide. The active IL-18  
 polypeptide has an activity of inducing the production of interferon  
 (IFN)-gamma in immunocompetent cells. IFN-gamma is useful as a  
 biologically active substance for stimulating the production of IFNg from  
 KG-1 (human myelomonocytic cell line) cells. The present sequence is  
 human active IL-18 protein  
 Sequence 157 AA;  
  
 Query Match 99.9%; Score 811; DB 5; Length 157;  
 Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
 DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
  
 QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSKSDIIFQSVPGHDNKMQFESSY 120  
 DB 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTSKSDIIFQSVPGHDNKMQFESSY 120  
  
 QY 121 EGYFLACEKERDLFKILKKEDELGDRSIMFTVQNE 157  
 DB 121 EGYFLACEKERDLFKILKKEDELGDRSIMFTVQNE 157  
  
 RESULT 9  
 ABG73359  
 ID ABG73359 standard; protein; 157 AA.  
 XX  
 AC ABG73359;  
 XX  
 DT 13-MAY-2003 (first entry)  
 XX  
 DE Human wild-type mature interleukin-18 (IL-18).  
 XX  
 KW Human; human interleukin-18; IL-18; IL-18 binding protein; IL-18BP;  
 KW T helper type I response; Th1 response; cancer; viral disease;  
 KW microbial infection; tumour immunotherapy; adjuvant; DNA vaccination;  
 KW graft versus tumour therapy; neutralisation; cytostatic; virucide;  
 KW antimicrobial.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002169291-A1.  
 XX  
 PD 14-NOV-2002.  
 XX  
 XX 08-MAR-2002; 2002US-00094153.  
 XX  
 PF 08-MAR-2001; 2001US-0274327P.  
 PR  
 XX (DINA/) DINARELLO C.  
 PA (KIMS/) KIM S H.  
 XX  
 PI Dinarello C, Kim SH;

XX WPI; 2003-298731/29.  
 DR N-PSDB; ABX11788.  
 XX  
 XX Novel interleukin-18 mutant polypeptide useful in the treatment of cancer  
 PT and viral disease, has mutations in amino acid residues which are  
 PT involved in its interaction with IL-18 binding protein.  
 XX  
 PS Example 1; Fig 1B; 23pp; English.  
 XX  
 CC The present invention relates to mutants of human interleukin-18 (IL-18)  
 CC protein that have a lower affinity for IL-18 binding protein (IL-18BP)  
 CC than the wild-type IL-18 protein. The IL-18 mutants of the invention  
 CC comprise mutations in one or more amino acid residues which are involved  
 CC in its interaction with IL-18BP. The mutations comprise substitutions,  
 CC preferably non-conservative, additions or deletions. A pharmaceutical  
 CC composition comprising an IL-18 mutant is useful for treating a disease  
 CC which is prevented or alleviated by a T helper type I (Th1) response,  
 CC including cancer and viral disease. The IL-18 mutants are useful in the  
 CC treatment of the above diseases, microbial infections, in tumour  
 CC immunotherapy, and as an adjuvant in DNA vaccination and in graft versus  
 CC tumour therapy. The IL-18 mutants are resistant to, or less susceptible  
 CC to, neutralisation than the wild-type protein. The present sequence  
 CC represents human wild-type mature IL-18 protein  
 XX  
 SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 6; Length 157;  
 Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTFIISMVKDSQPRGM 60  
 |||||  
 DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTFIISMVKDSQPRGM 60  
 |||||

QY 61 AVTISVKCKISLSCENKIISFKENPPDNINIKTSKDIIFFORSVPGHDNKKMOFFESSY 120  
 |||||  
 DB 61 AVTISVKCKISLSCENKIISFKENPPDNINIKTSKDIIFFORSVPGHDNKKMOFFESSY 120  
 |||||

QY 121 EGYFLACERDLFKLILKKEDELGRSINFTVQNEED 157  
 |||||  
 DB 121 EGYFLACERDLFKLILKKEDELGRSINFTVQNEED 157  
 |||||

RESULT 10  
 ADA50616  
 ID ADA50616 standard; protein; 157 AA.  
 XX  
 AC ADA50616;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 XX Human mature consensus interleukin-18 (IL-18), SEQ ID NO:71.  
 DE  
 DE Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;  
 KW humoral response; cellular response; immune response; immunotherapy;  
 KW cancer; cytostatic; vaccine; gene therapy; interleukin-18; IL-18; human.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 4  
 FT /note= "Glu may replace wild-type Lys in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 5  
 FT /note= "Val may replace wild-type Leu in a variant  
 FT protein. A variant protein with this substitution is  
 FT unlikely to have changed immunogenicity compared to the  
 FT wild-type protein"  
 FT  
 FT Misc-difference 6  
 FT /note= "Ile may replace wild-type Glu in a variant  
 FT protein. A variant protein with this substitution would

FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 8  
 FT /note= "Asp may replace wild-type Lys in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 10  
 FT /note= "Thr may replace wild-type Ser in a variant  
 FT protein. A variant protein with this substitution would  
 FT not have changed immunogenicity compared to the wild-type  
 FT protein"  
 FT  
 FT Misc-difference 12  
 FT /note= "Val may replace wild-type Ile in a variant  
 FT protein. A variant protein with this substitution would  
 FT not have changed immunogenicity compared to the wild-type  
 FT protein"  
 FT  
 FT Misc-difference 13  
 FT /note= "Ile may replace wild-type Arg in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 15  
 FT /note= "Arg may replace wild-type Leu in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 17  
 FT /note= "Lys may replace wild-type Asp in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 20  
 FT /note= "Val or Ile may replace wild-type Leu in a variant  
 FT protein. A variant protein with this substitution is  
 FT unlikely to have changed immunogenicity compared to the  
 FT wild-type protein"  
 FT  
 FT Misc-difference 21  
 FT /note= "Tyr may replace wild-type Phe in a variant  
 FT protein. A variant protein with this substitution is  
 FT unlikely to have changed immunogenicity compared to the  
 FT wild-type protein"  
 FT  
 FT Misc-difference 22  
 FT /note= "Val may replace wild-type Ile in a variant  
 FT protein. A variant protein with this substitution is  
 FT unlikely to have changed immunogenicity compared to the  
 FT wild-type protein"  
 FT  
 FT Misc-difference 27  
 FT /note= "Lys may replace wild-type Arg in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 30  
 FT /note= "Ala may replace wild-type Phe in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 35  
 FT /note= "Lys may replace wild-type Asp in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 37  
 FT /note= "Phe may replace wild-type Asp in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 38  
 FT /note= "Glu may replace wild-type Cys in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 39  
 FT /note= "Ala may replace wild-type Arg in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 40  
 FT /note= "Trp may replace wild-type Asp in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 45  
 FT /note= "Ser may replace wild-type Thr in a variant  
 FT protein. A variant protein with this substitution would

FT not have changed immunogenicity compared to the wild-type  
FT protein"  
FT Misc-difference 47  
FT /note= "Tyr may replace wild-type Phe in a variant  
FT protein. A variant protein with this substitution would  
FT not have changed immunogenicity compared to the wild-type  
FT protein"  
FT Misc-difference 51  
FT /note= "Glu may replace wild-type Met in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 52  
FT /note= "Phe may replace wild-type Tyr in a variant  
FT protein. A variant protein with this substitution would  
FT not have changed immunogenicity compared to the wild-type  
FT protein"  
FT Misc-difference 53  
FT /note= "Gly may replace wild-type Lys in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 56  
FT /note= "Ile may replace wild-type Glp in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 58  
FT /note= "Ala may replace wild-type Arg in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 62  
FT /note= "Lys may replace wild-type Val in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 64  
FT /note= "Val may replace wild-type Ile in a variant  
FT protein. A variant protein with this substitution would  
FT not have changed immunogenicity compared to the wild-type  
FT protein"  
FT Misc-difference 94  
FT /note= "Lys may replace wild-type Asp in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 95  
FT /note= "Phe may replace wild-type Thr in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 101  
FT /note= "Tyr may replace wild-type Phe in a variant  
FT protein. A variant protein with this substitution would  
FT not have changed immunogenicity compared to the wild-type  
FT protein"  
FT Misc-difference 104  
FT /note= "Leu may replace wild-type Arg in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 108  
FT /note= "Ile may replace wild-type Gly in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 111  
FT /note= "Lys may replace wild-type Asn in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 129  
FT /note= "Phe may replace wild-type Lys in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 131  
FT /note= "Asp may replace wild-type Arg in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 132  
FT /note= "Leu may replace wild-type Asp in a variant  
FT protein. A variant protein with this substitution would

FT Misc-difference 133  
FT /note= "Glu may replace wild-type Leu in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 134  
FT /note= "Ala may replace wild-type Phe in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT WO2003031569-A2.  
FT 17-APR-2003.  
FT 18-SEP-2002; 2002WO-US029640.  
FT 10-OCT-2001; 2001US-0328371P.  
FT (CENZ ) CENTOCOR INC.  
FT Snyder L, Scallon B, Knight DM, Mccarthy SG, Goletz TJ;  
FT Branigan PJ;  
FT WPI; 2003-393437/37.  
FT N-PSDB; ADA50613.  
FT New nucleic acid vaccine, useful for eliciting an immune response to a  
FT  
Query Match 99.9%; Score 811; DB 6; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISMYKDSQPRGM 60  
Qy 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQKRSVFGHDNKMQFESSY 120  
Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQKRSVFGHDNKMQFESSY 120  
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSINFVTQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFVTQNE 157  
RESULT 11  
ADA50610  
ID ADA50610 standard; protein; 157 AA.  
XX ADA50610;  
XX 20-NOV-2003 (first entry)  
DT Human mature consensus interleukin-18 (IL-18), SEQ ID NO:65.  
DE Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;  
XX humoral response; cellular response; immune response; immunotherapy;  
KW cancer; cytostatic; vaccine; gene therapy; interleukin-18; IL-18; human.  
XX Homo sapiens.  
OS  
XX WO2003031569-A2.  
PN 17-APR-2003.  
PD 18-SEP-2002; 2002WO-US029640.  
PF 10-OCT-2001; 2001US-0328371P.  
PR (CENZ ) CENTOCOR INC.  
XX Snyder L, Scallon B, Knight DM, Mccarthy SG, Goletz TJ;  
PI Branigan PJ;

XX WPI; 2003-393437/37.  
DR N-ESDB; ADA50608.  
XX  
XX New nucleic acid vaccine, useful for eliciting an immune response to a  
PT cancer associated tumor protein in a mammal.  
PT  
XX Claim 1b; Page 51-52; 92pp; English.  
PS  
XX The invention relates to a nucleic acid vaccine comprising one or more  
CC tumor antigen-encoding nucleic acids and one or more cytokine adjuvant-  
CC encoding nucleic acids. The tumor antigen encoded by the vaccine is  
CC mucin 1 (MUC-1), the kallikrein KLK2, or prostate specific antigen (PSA,  
CC also known as KUK3), and the cytokine adjuvant encoded can be interleukin  
CC -12 (IL-12), granulocyte macrophage-colony stimulating factor (GM-CSF),  
CC or especially interleukin-18 (IL-18). The antigen-encoding nucleic acid  
CC is preferably under the control of a promoter such as the cytomegalovirus  
CC immediate early promoter, the dihydrofolate reductase promoter or the  
CC early or late SV40 promoters. The invention also encompasses the method  
CC of eliciting an immune response to a tumour antigen in a mammal using the  
CC vaccine of the invention. Coexpression of the antigen and adjuvant  
CC induces a humoral or cellular response to the tumour antigen, generating  
CC an immune response useful for treatment or prophylaxis of cancers. The  
CC present sequence represents an interleukin-18 (IL-18) polypeptide which  
CC is specifically claimed for use in the vaccine of the invention.  
XX  
SQ Sequence 157 AA;  
Query Match 99.9%; Score 811; DB 6; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCKENKIIISFKEMNPPDNIKDTKSDIIFORSVPGHDKMKOFESSY 120  
Db 61 AVTISVKCEKISTLSCKENKIIISFKEMNPPDNIKDTKSDIIFORSVPGHDKMKOFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
RESULT 13  
ABR83372  
ID ABR83372 standard; protein; 157 AA.  
XX ABR83372;  
AC ABR83372;  
XX  
DT 07-OCT-2003 (first entry)  
XX Human interleukin 18 amino acid sequence.  
DE  
XX Human; interleukin 1; IL-1; interleukin 18; IL-18; mutant; mutein;  
KW mutant interleukin 18; MUT-IL-18; antiinflammatory; gene therapy;  
KW inflammatory disorder.  
XX  
XX Homo sapiens.  
OS  
XX WO2003057821-A2.  
FN  
XX 17-JUL-2003.  
PD  
XX 25-OCT-2002; 2002WO-US034235.  
PF  
XX 26-OCT-2001; 2001US-0335880P.  
PR  
XX (CENZ ) CENTOCOR INC.  
PA Heavner GA, Snyder LA, McCarthy SG;  
PI  
XX

DR WPI; 2003-577517/54.  
XX  
XX New MUT-IL-18 nucleic acid, useful for preparing a composition for  
PT diagnosing or treating a MUT-IL-18 related condition, e.g., inflammatory  
PT disorder.  
XX  
PS Example 3; Page 74; 97pp; English.  
XX  
XX The present invention describes a mutant interleukin 18 (MUT-IL-18)  
CC nucleic acid comprising or complementary to at least one polynucleotide  
CC encoding an IL-18 amino acid sequence comprising at least one mutation  
CC corresponding to at least one substitution selected from the group  
CC consisting of Thr10 for Ser10, Val12 for Ile12, Ser45 for Thr45, Tyr47  
CC for Phe47, Phe52 for Tyr52, Val64 for Ile64, Tyr101 for Phe101, Val15 for  
CC Leu15, Val20 for Leu20, Ile20 for Leu20, Tyr21 for Phe21, Val22 for Ile22,  
CC Ile66 for Val66, Thr72 for Ser72, or Phe148 for Ser148. Also described:  
CC (1) a MUT-IL-18 polypeptide; (2) a MUT-IL-18 antibody; (3) a MUT-IL-18  
CC vector comprising the MUT-IL-18 nucleic acid; (4) a MUT-IL-18 host cell  
CC comprising the MUT-IL-18 nucleic acid; (5) a composition comprising a MUT  
CC -IL-18 nucleic acid, polypeptide or antibody; (6) diagnosing or treating  
CC a MUT-IL-18 related condition in a cell, tissue, organ or animal; (7) a  
CC device comprising MUT-IL-18 nucleic acid, polypeptide or antibody and  
CC that is suitable for contacting or administering the MUT-IL-18 nucleic  
CC acid, polypeptide or antibody; (8) an article of manufacture for human  
CC pharmaceutical or diagnostic use; and (9) producing the MUT-IL-18 nucleic  
CC acid, polypeptide or antibody. MUT-IL-18 has antiinflammatory activity  
CC and can be used in gene therapy. The MUT-IL-18 nucleic acid can be used  
CC for preparing a composition for diagnosing or treating a MUT-IL-18  
CC related condition, e.g. inflammatory disorder. The present sequence  
CC represents a human IL-18 amino acid sequence given in an example from the  
CC present invention  
XX  
SQ Sequence 157 AA;  
Query Match 99.9%; Score 811; DB 6; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCKENKIIISFKEMNPPDNIKDTKSDIIFORSVPGHDKMKOFESSY 120  
Db 61 AVTISVKCEKISTLSCKENKIIISFKEMNPPDNIKDTKSDIIFORSVPGHDKMKOFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
RESULT 13  
ADE06775  
ID ADE06775 standard; protein; 157 AA.  
XX ADE06775;  
AC ADE06775;  
XX  
DT 29-JAN-2004 (first entry)  
XX Human anti-diabetes Ig derived protein SEQ ID NO:3.  
DE  
XX human; Ig; diabetes; complementarity-determining region; CDR;  
KW antidiabetic; ophthalmological; neuroprotective; gene therapy;  
KW diabetes mellitus; insulin resistance; hyperglycaemia; hypoglycaemia;  
KW pancreatitis; Cushing's syndrome; acanthosis nigricans; retinopathy;  
KW nephropathy; polyneuropathy; ulcer; infection.  
XX  
XX Homo sapiens.  
OS  
XX WO2003083071-A2.  
FN  
XX 09-OCT-2003.  
PD  
XX



PF 26-MAR-2003; 2003WO-US009459.  
XX  
PR 26-MAR-2002; 2002US-0367902P.  
XX  
PA (CENZ ) CENTOCOR INC.  
XX  
PI Griswold DE, Li J, Li L;  
XX  
XX WPI; 2003-804047/75.  
DR  
XX  
PT New isolated anti-diabetes immunoglobulin (Ig)-derived protein,  
PT comprising at least one complementarity determining region (CDR) useful  
PT for treating a diabetes-related condition, e.g. type I or II diabetes  
PT mellitus, retinopathy.  
XX  
XX Claim 1; SEQ ID NO 3; 84pp; English.  
XX  
XX The invention relates to a novel isolated anti-diabetes immunoglobulin  
XX (Ig)-derived protein, comprising at least one complementarity-determining  
XX region (CDR). A protein of the invention has antidiabetic,  
XX ophthalmological, and neuroprotective activity, and may have a use in  
XX gene therapy. The protein, nucleic acid, composition and methods of the  
XX invention are useful for treating a diabetes-related condition, e.g. type  
XX I or II diabetes mellitus, insulin resistance, hyperglycaemia,  
XX hypoglycaemia, pancreatitis, Cushing's syndrome, acanthosis nigricans,  
XX retinopathy, nephropathy, polyneuropathy, ulcers, or infections. The  
XX present sequence represents an anti-diabetes Ig derived protein of the  
XX invention.  
XX  
SQ Sequence 157 AA;  
  
Query Match 99.9%; Score 811; DB 7; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60  
  
QY 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKDTSIIFFQSVPGHDNMQFESSY 120  
DB 61 AVTISVKCEKISTLSCEKNKIIISFKEMNPPDNIKDTSIIFFQSVPGHDNMQFESSY 120  
  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
  
RESULT 14  
ADH54826  
ID ADH54826 standard; protein; 157 AA.  
XX  
XX ADH54826;  
AC  
XX  
XX 25-MAR-2004 (first entry)  
DT  
XX  
XX Human interleukin-18 (IL-18).  
DE  
XX  
XX Human; interleukin-18; IL-18; interferon-gamma-inducing factor; IGIF;  
KW Thi-inducer; cytokine; cell-mediated immunity; prevention;  
KW inflammatory bowel disease; IBD; Crohn's disease; ulcerative colitis;  
KW inflammatory colitis; antiinflammatory; gastrointestinal.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004002519-A1.  
PN  
XX  
XX 08-JAN-2004.  
FD  
XX  
XX 05-JUN-2003; 2003WO-US017744.  
PF  
XX  
XX 27-JUN-2002; 2002US-0392176P.  
PR  
XX

PA (SMIX ) SMITHKLINE BEECHAM CORP.  
XX  
XX Goto Y, Kikkawa H, Kinoshita M;  
XX  
XX WPI; 2004-099186/10.  
DR  
XX  
XX Preventing and/or treating inflammatory bowel diseases caused by  
PT bacteria, ischemia, radiation, drugs or chemical substances comprises  
PT administering an interferon-gamma-inducing factor (IGIF), interleukin-18.  
XX  
XX Claim 1; SEQ ID NO 1; 20pp; English.  
XX  
XX The invention relates to a method of treating or preventing inflammatory  
XX bowel disease (IBD) by administering human or murine interleukin-18 (IL-  
XX 18; ADH54826-ADH54827). The invention also relates to a pharmaceutical  
XX composition comprising human or murine IL-18 for treating or preventing  
XX IBD. IL-18 (also known as interferon-gamma-inducing factor (IGIF)) is a  
XX potent Thi-inducing cytokine and thus plays a key role in cell-mediated  
XX immunity. The methods and compositions of the invention are useful for  
XX the prevention and/or treatment of IBD, including Crohn's disease,  
XX ulcerative colitis and inflammatory colitis caused by bacteria, ischemia,  
XX radiation, drugs or chemical substances. The present sequence represents  
XX human IL-18 which is specifically claimed for use in the methods and  
XX compositions of the invention.  
XX  
SQ Sequence 157 AA;  
  
Query Match 99.9%; Score 811; DB 8; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60  
  
QY 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKDTSIIFFQSVPGHDNMQFESSY 120  
DB 61 AVTISVKCEKISTLSCEKNKIIISFKEMNPPDNIKDTSIIFFQSVPGHDNMQFESSY 120  
  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
  
RESULT 15  
ADL24279  
ID ADL24279 standard; protein; 157 AA.  
XX  
XX ADL24279;  
AC  
XX  
XX 03-JUN-2004 (first entry)  
DT  
XX  
XX Human IL-18 ICE-processed.  
DE  
XX  
XX cardiovascular disease; IL-17; interleukin; IL-18; 4-1BB; CD30; OX40;  
KW antagonist.  
KW  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004019866-A2.  
PN  
XX  
XX 11-MAR-2004.  
FD  
XX  
XX 21-AUG-2003; 2003WO-US026354.  
PF  
XX  
XX 28-AUG-2002; 2002US-0406418P.  
PR  
XX  
XX 12-AUG-2003; 2003US-0494457P.  
XX  
XX (IMMV ) IMMUNEX CORP.  
PA  
XX  
XX Burton PB, Deisher TA;  
PI  
XX  
XX WPI; 2004-239107/22.  
DR

XX Use of IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists, for treating a  
PT cardiovascular disease, e.g. chronic immune myocarditis, congestive heart  
PT failure, aneurysm, angina, embolism, restenosis, ischemia or  
PT thrombocytopenic purpura.  
XX  
PS Disclosure; Page 112; 135pp; English.  
XX  
CC The present invention relates to a method of treating cardiovascular  
CC disease in a subject, comprising administering an IL-17, IL-18, 4-1BB,  
CC CD30 or OX40 antagonist. The IL-17, IL-18, 4-1BB, CD30 or OX40  
CC antagonists are useful for treating cardiovascular disorders, e.g.  
CC (chronic immune) myocarditis, congestive heart failure, aneurysms,  
CC angina, embolism, restenosis, ischaemia or thrombocytopenic purpura. The  
CC present sequence is a polypeptide used in the exemplification of the  
CC invention.  
XX  
SQ Sequence 157 AA;  
Query Match 99.9%; Score 811; DB 8; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60  
QY -61 AVTISVKCEKISLSCENKIISPKEMNPPDNIKDTKSDIIFORSVPGHDKMKQFESSY 120  
DB 61 AVTISVKCEKISLSCENKIISPKEMNPPDNIKDTKSDIIFORSVPGHDKMKQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Search completed: January 30, 2006, 08:37:18  
Job time : 137 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2006, 08:48:54 ; Search time 167 Seconds  
(without alignments)  
663.281 Million cell updates/sec

Title: US-09-716-356A-6  
Perfect score: 157  
Sequence: 1 YFGKLESLVIRNLNDQVL.....LKKEDELGDRSIMFTVQNEED 157

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	53.5	189	2	Q6WJ17_HUMAN
2	84	53.5	193	1	IL18_HUMAN
3	84	53.5	193	2	Q6FGF3_HUMAN
4	55	35.0	193	2	Q96KJ8_HUMAN
5	54	34.4	193	2	Q9BG15_MACMU
6	39	24.8	45	2	Q9NQ49_HUMAN
7	19	12.1	159	2	Q6QVC4_CAPI
8	19	12.1	193	2	Q9GL09_SHEEP
9	14	8.9	178	2	Q9MZL8_BOVIN
10	14	8.9	193	1	IL18_BOVIN
11	14	8.9	193	2	Q5I931_BOSTR
12	14	8.9	193	2	Q6TLW4_BUBBU
13	14	8.9	193	2	Q6T573_BUBBU
14	13	8.3	177	2	Q6STL7_PIG
15	13	8.3	192	1	IL18_PIG
16	13	8.3	192	2	Q865B8_FELCA
17	13	8.3	192	2	Q9N1P7_PIG
18	13	8.3	192	2	Q95M33_FELCA
19	13	8.3	193	1	IL18_CANFA
20	13	8.3	193	1	IL18_HORSE
21	10	6.4	84	2	Q95LE7_CANFA
22	8	5.1	195	2	Q80Y07_MERUN
23	8	5.1	660	2	Q5T9T7_HUMAN
24	8	5.1	893	2	Q8D555_HUMAN
25	8	5.1	1139	1	ARHGA_HUMAN
26	8	5.1	2175	2	Q5S003_MOUSE
27	8	5.1	2223	2	Q6Q759_HUMAN
28	8	5.1	5890	2	Q8IK84_PLAF7
29	7	4.5	61	2	Q6IGT1_DROME
30	7	4.5	128	2	Q4JAC8_SULAC
31	7	4.5	144	2	Q77LV3_9NUCL

32	7	4.5	144	2	Q9E215_9NUCL
33	7	4.5	144	2	Q9IFI9_9NUCL
34	7	4.5	145	2	Q9HLS4_TREAC
35	7	4.5	151	2	Q8CZ29_STRRG
36	7	4.5	151	2	Q97821_STRPN
37	7	4.5	158	2	Q98Y88_GUITH
38	7	4.5	164	2	Q4FT23_9THEM
39	7	4.5	170	2	Q5AR78_EMENI
40	7	4.5	181	2	Q620C0_CAEBR
41	7	4.5	188	2	Q34259_9HEMI
42	7	4.5	189	2	Q35368_9HEMI
43	7	4.5	189	2	Q80S88_MOUSE
44	7	4.5	190	2	Q8WBS8_9HEMI
45	7	4.5	192	1	IL18_MOUSE
46	7	4.5	192	2	Q6USQ6_MOUSE
47	7	4.5	196	2	Q91266_SIGHI
48	7	4.5	206	2	Q81UB6_BACAN
49	7	4.5	212	2	Q612K1_BACAN
50	7	4.5	221	2	Q4XGS4_PLACH
51	7	4.5	231	2	Q6YIH6_MYRFP
52	7	4.5	242	2	Q73LC6_TREDE
53	7	4.5	246	2	Q82652_ARATH
54	7	4.5	254	2	Q91FD9_IRV6
55	7	4.5	259	2	Q4Z9D4_9CAUD
56	7	4.5	264	2	Q4ZXZ7_PSESY
57	7	4.5	268	2	Q7VJ34_PROMP
58	7	4.5	275	2	Q4IRQ9_GIBZE
59	7	4.5	285	2	Q7UE74_RHOBA
60	7	4.5	295	2	Q76407_CAEEL
61	7	4.5	322	2	Q9KEQ4_BACHD
62	7	4.5	334	2	Q74M41_NANEO
63	7	4.5	326	2	Q97UH2_SULSO
64	7	4.5	329	2	Q9GQ96_PLAFA
65	7	4.5	332	2	Q9CJT5_PASMU
66	7	4.5	333	2	Q9GQ94_PLAFA
67	7	4.5	334	2	Q92XB4_RHIME
68	7	4.5	334	2	Q835H8_ENTFA
69	7	4.5	366	2	Q8RA01_THETN
70	7	4.5	390	2	Q8FUG3_ECOL6
71	7	4.5	393	2	Q6AAL3_PROAC
72	7	4.5	417	2	Q5FL86_LACAC
73	7	4.5	429	1	ENO_ANAP
74	7	4.5	431	2	Q5N8S8_ORYSA
75	7	4.5	432	1	ENO_SYNY3
76	7	4.5	435	2	Q6FIR7_MESFL
77	7	4.5	449	2	Q7TTV6_SYNPX
78	7	4.5	458	2	Q22803_ARATH
79	7	4.5	465	2	Q8VY01_ARATH
80	7	4.5	484	2	Q7PXA5_ANGOA
81	7	4.5	496	2	Q5JMA8_ORYSA
82	7	4.5	510	2	Q73F86_MYCPA
83	7	4.5	525	2	Q8IIC0_PLAF7
84	7	4.5	525	2	Q7WT34_9ACTO
85	7	4.5	547	2	Q4SPA4_TETNG
86	7	4.5	548	2	Q9RA74_STRDY
87	7	4.5	552	1	NCAP_TPMV
88	7	4.5	557	2	Q7XVA4_ORYSA
89	7	4.5	589	2	Q8WM81_CAEEL
90	7	4.5	612	2	Q5HBG0_EHRW
91	7	4.5	614	2	Q73RP0_TREDE
92	7	4.5	618	2	Q5ATS8_EMENI
93	7	4.5	623	2	Q6LK80_PHOFR
94	7	4.5	624	2	Q9UJN7_CAEEL
95	7	4.5	633	2	Q5FHN3_EHRW
96	7	4.5	633	2	Q5FDV4_EHRW
97	7	4.5	641	1	LICR_BACSU
98	7	4.5	645	2	Q6CYA8_KLULA
99	7	4.5	653	2	Q4FVAL_9GAMW
100	7	4.5	653	2	Q6F741_AC1AD

ALIGNMENTS

```

RESULT 1
ID Q6WJ7 HUMAN PRELIMINARY; PRT; 189 AA.
AC Q6WJ7;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE DELTA3PRO-IL-18.
GN Name=IL18;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaggero A., De Ambrosis A., Mezzanzanica D., Piazza T., Rubartelli A.,
RA Figini M., Canevari S., Ferrini S.;
RA "A novel isoform of pro-interleukin-18 expressed in ovarian tumors is
RT resistant to caspase-1 and -4 processing.";
RL Oncogene 0:0-0(2004).
DR EMBL; AY266351; AAP92112.1; -; mRNA.
DR SRR; Q6WJ7; 33-189.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SRR; Q6WJ7; 33-189.
SQ SEQUENCE 189 AA; 21896 MW; A8BA275CF713A4B6 CRC64;

Query Match 53.5%; Score 84; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 3.1e-83;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIIIFKEMPPDNKIDKTSIDIFPORSVPGHNDKMQPSSSYEGYFLACEKERDL 133
Db 106 LSCENKIIIFKEMPPDNKIDKTSIDIFPORSVPGHNDKMQPSSSYEGYFLACEKERDL 165

QY 134 FKILKKEDLGRSMFTVQNEED 157
Db 166 FKILKKEDLGRSMFTVQNEED 189

RESULT 2
IL18_HUMAN STANDARD; PRT; 193 AA.
AC Q14116; O75599;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN Name=IL18; Synonyms=IGIF, IL1F4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
RA Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,
RA Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
RT "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
RT in Escherichia coli, and studies on the biologic activities of the
RL protein.";
RL J. Immunol. 156:4274-4279(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Yong D., Guixin D., Lihua H., Haitao W.;
RT "Cloning and sequencing of the cDNA for precursor hIL-18.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Liu J., Peng X., Yuan J., Qiang B.;
RT "Cloning of human interleukin 18 cDNA.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA TISSUE=Urinary bladder;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE OF 2-193.
RC TISSUE=Peripheral blood;
RA Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Augments natural killer cell activity in spleen cells
CC and stimulates interferon gamma production in T helper type I
CC cells.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; D49950; BAA08706.1; -; mRNA.
CC EMBL; AF077611; AAC27787.1; -; mRNA.
CC EMBL; AY044641; AAK95950.1; -; mRNA.
CC EMBL; BC007007; AAH07007.1; -; mRNA.
CC EMBL; BC007461; AAH07461.1; -; mRNA.
CC EMBL; U90434; AAB50010.1; -; mRNA.
CC FDB; J305; NMR; A=37-193.
CC OGP; Q14116; -.
CC Ensemble; ENSG00000150782; Homo sapiens.
CC HGNC; HGNC:5986; IL18.
CC H-InvDB; HIX0010123; -.
CC MIM; 600953; -.
CC GO; GO:0005576; C:extracellular region; TAS.
CC GO; GO:0005125; F:cytokine activity; TAS.
CC GO; GO:0004871; F:signal transducer activity; TAS.
CC GO; GO:0001525; P:angiogenesis; IDA.
CC GO; GO:0007267; P:cell-cell signaling; TAS.
CC GO; GO:0042033; P:chemokine biosynthesis; TAS.
CC GO; GO:0042233; P:granulocyte macrophage colony-stimulating f. .; TAS.
CC GO; GO:0006955; P:immune response; TAS.
CC GO; GO:0008625; P:induction of apoptosis via death domain rec. .; ISS.
CC GO; GO:0042095; P:interferon-gamma biosynthesis; TAS.
CC GO; GO:0042231; P:interleukin-13 biosynthesis; TAS.
CC GO; GO:0042094; P:interleukin-2 biosynthesis; TAS.
CC GO; GO:0042104; P:positive regulation of activated T cell pro. .; IDA.
CC GO; GO:0030155; P:regulation of cell adhesion; IDA.
CC GO; GO:0030431; P:sleep; ISS.
CC GO; GO:0042092; P:T-helper 2 type immune response; TAS.

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DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
KW 3D-structure; Cytokine.
FT PROPEP 1 36
FT CHAIN 37 193
FT CONFLICT 66 66
FT CONFLICT 86 86
FT CONFLICT 191 191
FT CONFLICT 191 191
SQ SEQUENCE 193 AA; 22326 MW; 323C62C203788D55 CRC64;
Query Match
Best Local Similarity 53.5%; Score 84; DB 1; Length 193;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 74 LSCENKIISFKEMNPPDNKDTKSDIIFQSRVPGHDKMQFESSYGYFLACEKERDL 133
DB 110 LSCENKIISFKEMNPPDNKDTKSDIIFQSRVPGHDKMQFESSYGYFLACEKERDL 169
QY 134 FKLLKKEDELGDRSIMFTVQNE 157
DB 170 FKLLKKEDELGDRSIMFTVQNE 193
RESULT 3
Q6FGY3 HUMAN
ID Q6FGY3_HUMAN PRELIMINARY; PRT; 193 AA.
AC Q6FGY3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE IL18 protein.
GN Name=IL18;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR541973; CAG46771.1; -; mRNA.
DR EMBL; CR542001; CAG46798.1; -; mRNA.
SQ SEQUENCE 193 AA; 22326 MW; 323C62C203788D55 CRC64;
Query Match
Best Local Similarity 53.5%; Score 84; DB 2; Length 193;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 74 LSCENKIISFKEMNPPDNKDTKSDIIFQSRVPGHDKMQFESSYGYFLACEKERDL 133
DB 110 LSCENKIISFKEMNPPDNKDTKSDIIFQSRVPGHDKMQFESSYGYFLACEKERDL 169
QY 134 FKLLKKEDELGDRSIMFTVQNE 157
DB 170 FKLLKKEDELGDRSIMFTVQNE 193
RESULT 4
Q96KJ8 HUMAN
ID Q96KJ8_HUMAN PRELIMINARY; PRT; 193 AA.
AC Q96KJ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ying P., Jianxin L.,
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF380360; AAK57024.1; -; mRNA.
DR HSP; Q14116; IJ08.
DR SMR; Q96KJ8; 37-193.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005149; P:interleukin-1 receptor binding; IEA.
DR GO; GO:0006985; P:immune response; IEA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;
Query Match
Best Local Similarity 35.0%; Score 55; DB 2; Length 193;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 QVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGMVATISVKCEKIS 72
DB 54 QVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGMVATISVKCEKIS 108
RESULT 5
Q9BG15 MACMU
ID Q9BG15_MACMU PRELIMINARY; PRT; 193 AA.
AC Q9BG15;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin-18.
GN Name=IL18;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=2129850; PubMed=11311040; DOI=10.1089/107999001750133212;
RA Giavedoni L.D., Imhoof J.D., Parodi L.M., Velasquillo C.M.,
RA Hodara V.L.;
RT "Expression of the interleukin-18 gene from rhesus macaque by the
RT simian immunodeficiency virus does not result in increased viral
RT replication."
RL J. Interferon Cytokine Res. 21:173-180(2001).
DR EMBL; AF303732; AAK13416.1; -; mRNA.
DR HSP; Q14116; IJ08.
DR SMR; Q9BG15; 37-193.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
SQ SEQUENCE 193 AA; 22325 MW; B2BD29C033BB0B5E CRC64;
Query Match
Best Local Similarity 34.4%; Score 54; DB 2; Length 193;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 80 IISFKEMNPPDNKDTKSDIIFQSRVPGHDKMQFESSYGYFLACEKERDL 133
DB 116 IISFKEMNPPDNKDTKSDIIFQSRVPGHDKMQFESSYGYFLACEKERDL 169
RESULT 6
Q9NQ49 HUMAN
ID Q9NQ49_HUMAN PRELIMINARY; PRT; 45 AA.
AC Q9NQ49;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin-18 (Fragment).
GN Name=IL-18;
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OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Farhan A.J., Pravica V., Hutchinson I.V.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ295724; CAC01436.1; -; Genomic_DNA.
DR HSSP; Q14116; 1J0S.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
FT NON_TER 1 45
FT NON_TER 45 45
SQ SEQUENCE 45 AA; 5266 MW; DF3A626507E3D61A CRC64;

Query Match 24.8%; Score 39; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSR 39
|
Db 7 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSR 45

RESULT 7
Q6QVC4 CAPHI
ID Q6QVC4 CAPHI PRELIMINARY; PRT; 159 AA.
AC Q6QVC4;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Interleukin-18 (Fragment).
GN Name=il-18;
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Liu W., Sui Z., Zhao H.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY524275; AAS13327.1; -; mRNA.
DR SMR; Q6QVC4; 3-159.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 159 AA; 18331 MW; FDCDEAAF15278FFC CRC64;

Query Match 12.1%; Score 19; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 4.9e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNI 92
|
Db 76 LSCENKIISFKEMNPPDNI 94

RESULT 8
Q9GL09 SHEEP
ID Q9GL09 SHEEP PRELIMINARY; PRT; 193 AA.
AC Q9GL09;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Interleukin-18 (IGIF).
GN Name=il-18;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

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OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bailey S.L., Gossner A., Dalziel R., Hopkins J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ401033; CAC09326.2; -; mRNA.
DR HSSP; Q14116; 1J0S.
DR SMR; Q9GL09; 37-193.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 193 AA; 22166 MW; CCD0A329062EF18C CRC64;

Query Match 12.1%; Score 19; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 5.9e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNI 92
|
Db 110 LSCENKIISFKEMNPPDNI 128

RESULT 9
Q9MZL8 BOVIN
ID Q9MZL8 BOVIN PRELIMINARY; PRT; 178 AA.
AC Q9MZL8;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Interleukin-18 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Olsen S.C., Lee I.K., Mwangi S.M., Kehrli M., Bolin C.A.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF173175; AAF89833.1; -; mRNA.
DR HSSP; Q14116; 1J0S.
DR SMR; Q9MZL8; 22-178.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
FT NON_TER 1 1
FT NON_TER 178 178
SQ SEQUENCE 178 AA; 20631 MW; 816D6B2B88ACB497 CRC64;

Query Match 8.9%; Score 14; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 SDIIFQRSVPGHD 110
|
Db 118 SDIIFQRSVPGHD 131

RESULT 10
ILL18 BOVIN
ID ILL18 BOVIN STANDARD; PRT; 193 AA.
AC Q9TU73;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)

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DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)  
 DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).  
 GN Name=IL18;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20012648; PubMed=10547157; DOI=10.1089/1079990993131118;  
 RA Shoda L.K., Zarlega D.S., Hirano A., Brown W.C.;  
 RT "Cloning of a cDNA encoding bovine Interleukin-18 and analysis of IL-  
 RT 18 expression in macrophages and its IFN-gamma-inducing activity.";  
 RL J. Interferon Cytokine Res. 19:1169-1177(1999).  
 CC -!- FUNCTION: Augments natural killer cell activity in spleen cells  
 CC and stimulates interferon gamma production in T helper type I  
 CC cells (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-1 family.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC EMBL; AF124789; AAF08686.1; -; mRNA.  
 DR SMR; Q9TU73; 37-193.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR Pfam; PF00340; IL1; 1.  
 DR SMART; SM00125; IL1; 1.  
 KW Cytokine.  
 FT PROPEP  
 FT CHAIN 1 36 By similarity.  
 FT CHAIN 37 193 Interleukin-18.  
 SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

Query Match 8.9%; Score 14; DB 1; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 SDIIFQSVPGHD 110  
 |||||  
 DB 133 SDIIFQSVPGHD 146

RESULT 11  
 Q51931\_BOSTR PRELIMINARY; PRT; 193 AA.  
 ID Q51931\_BOSTR PRELIMINARY; PRT; 193 AA.  
 AC Q51931;  
 DT 10-MAY-2005 (TREMBLrel. 30, Created)  
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)  
 DE Interleukin-18.  
 OS Boselaphus tragocamelus (Nilgai).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Boselaphus.  
 OX NCBI\_TaxID=9917;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Saini M., Swarup D., Yadav M.P., Singh G.R., Arora B.M., Chandra P.,  
 RA Das D.K., Gupta P.K.;  
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY842499; AAW34191.1; -; mRNA.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR Pfam; PF00340; IL1; 1.  
 SQ SEQUENCE 193 AA; 22130 MW; 75B6671696EEA48D CRC64;

Query Match 8.9%; Score 14; DB 2; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 SDIIFQSVPGHD 110  
 |||||  
 DB 133 SDIIFQSVPGHD 146

RESULT 12  
 Q6TLW4\_BUBBU PRELIMINARY; PRT; 193 AA.  
 ID Q6TLW4\_BUBBU PRELIMINARY; PRT; 193 AA.  
 AC Q6TLW4;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Interleukin 18.  
 GN Name=IL18;  
 OS Bubalus bubalis (Domestic water buffalo).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bubalus.  
 OX NCBI\_TaxID=89462;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Chaudhuri P., Bera B.C.;  
 RT "Cloning and sequencing of Indian water buffalo interleukin-18 cDNA.";  
 RL Eur. J. Immunogenet. 32:75-78(2005).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.

RA Chaudhuri P., Bera B.C.;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY394479; NAO94552.1; -; mRNA.  
 DR SMR; Q6TLW4; 37-193.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR Pfam; PF00340; IL1; 1.  
 SQ SEQUENCE 193 AA; 22176 MW; 66116F198DE94BC4 CRC64;

Query Match 8.9%; Score 14; DB 2; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 SDIIFQSVPGHD 110  
 |||||  
 DB 133 SDIIFQSVPGHD 146

RESULT 13  
 Q6T573\_BUBBU PRELIMINARY; PRT; 193 AA.  
 ID Q6T573\_BUBBU PRELIMINARY; PRT; 193 AA.  
 AC Q6T573;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Interleukin-18.  
 OS Bubalus bubalis (Domestic water buffalo).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bubalus.  
 OX NCBI\_TaxID=89462;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Premraj A., Sreskumar E., Rasool T.J.;  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY436506; AAR29081.1; -; mRNA.  
 DR SMR; Q6T573; 37-193.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR Pfam; PF00340; IL1; 1.  
 SQ SEQUENCE 193 AA; 22190 MW; 93103E5C62B745DE CRC64;

Query Match 8.9%; Score 14; DB 2; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 97 SDIFFORSVPGHD 110
Db 133 SDIFFORSVPGHD 146

RESULT 14
Q6STL7_PIG PRELIMINARY; PRT; 177 AA.
AC Q6STL7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Interleukin 18.
GN Names-IL-18;
OS Sus scrofa (Pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lu X., Hui L.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY450287; AAR27432.1; -; mRNA.
DR SNR; Q6STL7, 36-177.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
SQ SEQUENCE 177 AA; 20300 MW; 426F30330EB1F815 CRC64;

Query Match 8.3%; Score 13; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 98 DIIFORSVPGHD 110
Db 133 DIIFORSVPGHD 145

RESULT 15
IL18_PIG STANDARD; PRT; 192 AA.
AC Q19073;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN Name-IL18; Synonyms=IGIF;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Foss D.L., Murtaugh M.P.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Penha-Goncalves M.N., Logan N.A., Nicolson L., Onions D.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Muneta Y., Mori Y.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=20260994; PubMed=10803849; DOI=10.1007/s002510050630;
RA Fournout S., Dozois C.M., Yerle M., Pinton P., Fairbrother J.M.,
RA Oswald E., Oswald I.P.;
RT "Cloning, chromosomal location, and tissue expression of the gene for
RT pig interleukin-18."

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RL Immunogenetics 51:358-365(2000).
CC -!- FUNCTION: Augments natural killer cell activity in spleen cells
CC and stimulates interferon gamma production in T helper type 1
CC cells (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U68701; AAC18415.1; -; mRNA.
DR EMBL; Y11132; CAA72014.1; -; mRNA.
DR EMBL; AB010003; BAA24135.1; -; mRNA.
DR EMBL; AF191088; AAF71200.1; -; mRNA.
DR SMR; O19073; 36-192.
DR GO; GO:0005576; C:extracellular region; ISS.
DR GO; GO:0005125; P:cytokine activity; IMP.
DR GO; GO:0001525; P:angiogenesis; ISS.
DR GO; GO:0042033; P:chemokine biosynthesis; ISS.
DR GO; GO:0008625; P:induction of apoptosis via death domain rec. .; IDA.
DR GO; GO:0042095; P:interferon-gamma biosynthesis; IDA.
DR GO; GO:0042104; P:positive regulation of activated T cell pro. .; ISS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
DR Cytokine.
DR PROPEP 1 35 By similarity.
FT CHAIN 36 192 Interleukin-18.
FT SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;

Query Match 8.3%; Score 13; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 DIIFORSVPGHD 110
Db 133 DIIFORSVPGHD 145

RESULT 16
Q865B8_FELCA PRELIMINARY; PRT; 192 AA.
AC Q865B8;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Interferon gamma inducing factor precursor.
GN Name=fil-18;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kuwahara C., Kawakami K., Kishi M., Mochizuki M.;
RT "Feline interleukin-18."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB056857; BAC65243.1; -; mRNA.
DR HSSP; Q14116; IJ05.
DR SMR; Q865B8; 36-191.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR Signal.
FT SIGNAL 1 35 Potential.
FT SEQUENCE 192 AA; 22071 MW; 204F32D131588513 CRC64;

Query Match 8.3%; Score 13; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;

```



Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISPKEM 86  
|||||  
Db 109 LSCENKIISPKEM 121

## RESULT 17

Q9N1P7\_PIG  
ID Q9N1P7\_PIG PRELIMINARY; PRT; 192 AA.  
AC Q9N1P7;  
DT 01-OCT-2000 (TREMELrel. 15, Created)  
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE Interleukin-18.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
OC Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RX MEDLINE=20356335; PubMed=10901174;  
RA Oem J.K., Song H.J., Kang S.W., Jeong W.S.;  
RT "Cloning, sequencing, and expression of porcine interleukin-18 in  
RT Escherichia coli.";  
RL Mol. Cells 10:343-347 (2000).  
DR EMBL; AF176949; AAF3169.1; -; mRNA.  
DR HSSP; Q14116; 1J0S.  
DR SMR; Q9N1P7; 36-192.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR000975; Interleukin\_1.  
DR Pfam; PF00340; IL1; 1.  
DR SMART; SM00125; IL1; 1.  
SQ SEQUENCE 192 AA; 21969 MW; A51EB7A4E221A16D CRC64;

Query Match 8.3%; Score 13; DB 2; Length 192;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 DIIFQSVPGHD 110  
|||||  
Db 133 DIIFQSVPGHD 145

## RESULT 18

Q95M33\_FELCA  
ID Q95M33\_FELCA PRELIMINARY; PRT; 192 AA.  
AC Q95M33;  
DT 01-DEC-2001 (TREMELrel. 19, Created)  
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
DT 13-SEP-2005 (TREMELrel. 31, Last annotation update)  
DE Interferon-gamma inducing factor (IL-18).  
GN Name=IGIF;  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Felidae;  
OC Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC Hannon L., McGillivray C.P., Argyle D.J.A., Nicolson L., Onions D.E.;  
RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP Qiao J., Xia X., Yang S.;  
RT "Cloning and sequence analysis of feline IL-18 gene.";  
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Y13923; CAC42918.1; -; mRNA.  
DR EMBL; DQ100372; AAY96319.1; -; mRNA.

DR HSSP; Q14116; 1J0S.  
DR SMR; Q95M33; 36-192.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR000975; Interleukin\_1.  
DR Pfam; PF00340; IL1; 1.  
SQ SEQUENCE 192 AA; 22068 MW; 5878C3DAC7A43358 CRC64;

Query Match 8.3%; Score 13; DB 2; Length 192;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISPKEM 86  
|||||  
Db 109 LSCENKIISPKEM 121

## RESULT 19

IL18\_CANFA  
ID IL18\_CANFA STANDARD; PRT; 193 AA.  
AC Q9XSR0;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)  
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).  
GN Name=IL18; Synonyms=IGIF;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
OC Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99309818; PubMed=10380699; DOI=10.1007/s002510050532;  
RA Argyle D.J., McGillivray C., Nicolson L., Onions D.E.;  
RT "Cloning, sequencing, and characterization of dog interleukin-18.";  
RL Immunogenetics 49:541-543 (1999).  
CC -!- FUNCTION: Augments natural killer cell activity in spleen cells  
CC and stimulates interferon gamma production in T helper type I  
CC cells (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the IL-1 family.  
CC  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; Y11133; CAA72015.1; -; mRNA.  
DR SMR; Q9XSR0; 37-192.  
DR Ensembl; ENSCAFG0000013994; Canis familiaris.  
DR GO; GO:0005576; C:extracellular region; TAS.  
DR GO; GO:0005125; F:cytokine activity; TAS.  
DR GO; GO:0042033; P:chemokine biosynthesis; ISS.  
DR GO; GO:0008625; P:induction of apoptosis via death domain rec. .; IEP.  
DR GO; GO:0042095; P:interferon-gamma biosynthesis; IDA.  
DR GO; GO:0042104; P:positive regulation of activated T cell pro. .; ISS.  
DR InterPro; IPR000975; Interleukin\_1.  
DR Pfam; PF00340; IL1; 1.  
KW Cytokine.  
FT PROPEP 1 36 By similarity.  
FT CHAIN 37 193 Interleukin-18.  
SQ SEQUENCE 193 AA; 22037 MW; OD973E586F461F25 CRC64;

Query Match 8.3%; Score 13; DB 1; Length 193;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 DIIFQSVPGHD 110  
|||||

```
Db 134 DIIFFQSVPGHD 146
RESULT 20
IL18_HORSE
ID IL18_HORSE STANDARD; PRT; 193 AA.
AC Q9XSO7;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN Name=IL18; Synonyms=IGIF;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE
RA Nicolson L., Penha-Goncalves M.N., Keanie J.L., Logan N.A.,
RA Argyle D.J., Onions D.E.;
RT "Nucleotide sequence of equine interleukin 12 and 18 cDNAs.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Augments natural killer cell activity in spleen cells
CC and stimulates interferon gamma production in T helper type I
CC cells (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; Y11131; CAA72013.1; -; mRNA.
DR SNR; Q9XSO7; 37-193.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
KW Cytokine.
KW PROPEP
FT CHAIN 1 36 By similarity.
FT CHAIN 37 193 Interleukin-18.
SQ SEQUENCE 193 AA; 22058 MW; 4D81535E9004ECAF CRC64;
Query Match 8.3%; Score 13; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 98 DIIFFQSVPGHD 110
Db 134 DIIFFQSVPGHD 146
RESULT 21
Q95LE7_CANFA
ID Q95LE7_CANFA PRELIMINARY; PRT; 84 AA.
AC Q95LE7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE IL-18 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tissue=Blood;
RX MEDLINE=21589073; PubMed=11730929; DOI=10.1016/S0165-2427(01)00385-3;
RA Chamizo C., Rubio J.M., Moreno J., Alvar J.;
RT "Semi-quantitative analysis of multiple cytokines in canine peripheral
RT blood mononuclear cells by [correction of zby] a single tube RT-PCR.";
```

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RL Vet. Immunol. Immunopathol. 83:191-202 (2001).
DR EMBL; AF327900; AAL28920.1; -; mRNA.
DR HSSP; Q14116; 1JOS.
DR SMR; Q95LE7; 5-83.
DR Ensembl; ENSCAFG00000013994; Canis familiaris.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
FT NON_TER 1 84
FT NON_TER 84 84
SQ SEQUENCE 84 AA; 9568 MW; 19BD9E27F336774B CRC64;
Query Match 6.4%; Score 10; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 IRLNDQVLF 21
Db 16 IRLNDQVLF 25
RESULT 22
Q80Y07_MERUN
ID Q80Y07_MERUN PRELIMINARY; PRT; 195 AA.
AC Q80Y07;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin 18.
GN Name=IL18;
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Gerbillinae; Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Peritoneum;
RX MEDLINE=22593022; PubMed=12706898; DOI=10.1016/S0378-1119(03)00457-8;
RA Gaucher D., Chadee K.;
RT "Gerbil interleukin-18 and caspase-1: cloning, expression and
RT characterization.";
RL Gene 307:159-166 (2003).
DR EMBL; AY095932; AAM34434.1; -; mRNA.
DR HSSP; Q14116; 1JOS.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 195 AA; 22172 MW; C6P815317953154D CRC64;
Query Match 5.1%; Score 8; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 111 NKMQPSS 118
Db 147 NKMQPSS 154
RESULT 23
Q5T9Y7_HUMAN
ID Q5T9Y7_HUMAN PRELIMINARY; PRT; 660 AA.
AC Q5T9Y7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Novel protein (Fragment)
GN Name=RP4-776P7.2; ORFNames=RP4-776P7.2-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
```

OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Brown A.;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL139345; CAI22956.1; -; Genomic DNA.  
 DR EMBL; AL121993; CAI22736.1; -; Genomic DNA.  
 DR EMBL; AL121993; CAI22956.1; JOINED; Genomic DNA.  
 DR EMBL; AL139345; CAI22736.1; JOINED; Genomic DNA.  
 FT NON\_TER 1  
 SQ SEQUENCE 660 AA; 74350 MW; AEC06A510AD5D493 CRC64;  
 Query Match 5.1%; Score 8; DB 2; Length 660;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 137 ILKKEDEL 144  
 |||||  
 Db 273 ILKKEDEL 280

RESULT 24  
 Q68D55 HUMAN  
 ID Q68D55 HUMAN PRELIMINARY; PRT; 893 AA.  
 AC Q68D55;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hypothetical protein DKFZp686H0726.  
 GN Name=DKFZp686H0726;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC The German cDNA Consortium;  
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,  
 RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;  
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CR749570; CAH18365.1; -; mRNA.  
 DR GO; GO:0005096; F:GTPase activator activity; IEA.  
 DR InterPro; IPR000219; RhoGEF.  
 DR Pfam; PF00621; RhoGEF; 1.  
 DR SMART; SM00325; RhoGEF; 1.  
 DR PROSITE; PS50010; DH.2; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 893 AA; 100316 MW; F65D623C94EBEED CRC64;  
 Query Match 5.1%; Score 8; DB 2; Length 893;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 136 LILKKEDE 143  
 |||||  
 Db 794 LILKKEDE 801

RESULT 25  
 ARHGA HUMAN  
 ID ARHGA HUMAN STANDARD; PRT; 1139 AA.  
 AC O15013; O14665; Q8IWD9; Q8IY77;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Rho guanine nucleotide exchange factor 10.

GN Name=ARHGEF10; Synonyms=KIAA0294;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
 RC TISSUE=Brain;  
 RX MEDLINE=97349984; PubMed=9205841;  
 RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,  
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. VII.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro."  
 RL DNA Res. 4:141-150(1997).  
 RN [2]  
 RP SEQUENCE REVISION.  
 RX MEDLINE=22158633; PubMed=12168954;  
 RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;  
 RT "Construction of expression-ready cDNA clones for KIAA genes: manual  
 RT curation of 330 KIAA cDNA clones."  
 RL DNA Res. 9:99-106(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 2 AND 3).  
 RC TISSUE=Ductenium, and Prostate;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villaton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE OF 123-1139 (ISOFORM 4).  
 RC TISSUE=Brain;  
 RX PubMed=9311494;  
 RA Ranta S., Lehesjoki A.-E., de Fatima Bonaldo M., Knowles J.A.,  
 RA Hirvasniemi A., Ross B., de Jong P.J., Soares M.B., de la Chapelle A.,  
 RA Gilliam T.C.;  
 RT "High-resolution mapping and transcript identification at the  
 RT progressive epilepsy with mental retardation locus on chromosome 8p."  
 RL Genome Res. 7:887-896(1997).  
 RN [5]  
 RP FUNCTION, AND VARIANT SMCV ILE-127.  
 RX MEDLINE=22870321; PubMed=14508709; DOI=10.1086/378159;  
 RA Verhoeven K., De Jonghe P., Van de Putte T., Nelis E., Zwijsen A.,  
 RA Verpoorten N., De Vriendt E., Jacobs A., Van Gerwen V., Francis A.,  
 RA Ceuterick C., Huybroeck D., Timmerman V.;  
 RT "Slowed conduction and thin myelination of peripheral nerves  
 RT associated with mutant rho guanine-nucleotide exchange factor 10."  
 RL Am. J. Hum. Genet. 73:926-932(2003).  
 CC -!- FUNCTION: May play a role in developmental myelination of  
 CC peripheral nerves.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1;  
 CC IsoId=O15013-1; Sequence=Displayed;  
 CC Name=2;

```
CC IsoId=O15013-2; Sequence=VSP_010700, VSP_010701, VSP_010705,
CC VSP_010706;
CC Note=No experimental confirmation available;
CC Name=3;
CC IsoId=O15013-3; Sequence=VSP_010701, VSP_010702, VSP_010703;
CC Note=No experimental confirmation available;
CC Name=4;
CC IsoId=O15013-4; Sequence=VSP_010704;
CC Note=No experimental confirmation available;
CC -!- DiSEASE: Defects in ARHGGEF10 are the cause of slowed nerve
CC conduction velocity (SNCV) [MIM:608236]. Affected individuals
CC present a reduction in nerve conduction velocities without any
CC clinical signs of peripheral or central nervous system
CC dysfunction. SNCV inheritance is autosomal dominant.
CC -!- SIMILARITY: Contains 1 DH (DBL-homology) domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB002292; BAA20754.2; ALT_INIT; mRNA.
CC EMBL; BC036809; AAH36809.1; -; mRNA.
CC EMBL; BC040474; AAH40474.1; -; mRNA.
CC EMBL; AF009205; AAH71662.1; -; mRNA.
CC PIR; T03307; T03307.
CC DR Ensembl; ENSG00000104728; Homo sapiens.
CC DR HGNC; HGNC:14103; ARHGGEF10.
CC DR MIM; 608136; -.
CC DR MIM; 608236; -.
CC DR InterPro; IPR001331; GDS_CDC24.
CC DR InterPro; IPR000219; RhoGEF.
CC DR Pfam; PF00621; RhoGEF; 1.
CC DR SMART; SM00325; RhoGEF; 1.
CC DR PROSITE; PS00741; DH_1; FALSE_NEG.
CC DR PROSITE; PS50010; DH_2; 1.
CC KW Alternative splicing; Coiled coil; Disease mutation;
CC Guanine-nucleotide releasing factor.
CC FT DOMAIN 191 378
CC FT COILED 75 95 Potential.
CC FT COILED 104 124 Potential.
CC FT COILED 360 394 Potential.
CC FT COMPIAS 1041 1074 Ser-rich.
CC FT VARSPPLIC 1 21 MENPEEAIDVDVPRENSDSEP -> MHS (in isoform
CC 2).
CC FT FTId=VSP_010700.
CC FT Missing (in isoform 2 and isoform 3).
CC FT FTId=VSP_010701.
CC FT LSSGSRYLRSDDMIETVYNDRGEIVTKERVFMNDVL
CC CATV -> VERGFLQLYSKIIFALC (in isoform
CC 3).
CC FT FTId=VSP_010702.
CC FT Missing (in isoform 3).
CC FT FTId=VSP_010703.
CC FT Missing (in isoform 4).
CC FT FTId=VSP_010704.
CC FT IGSCTHMQGIAIVSFQNSPKVIECNVESRILCMLYPVV
CC EEKRRFPAPPDPETPAVRASDPTICVGTTEG -> VRCV
CC YLVLVOVHRESTFMVGWMD (in isoform 2).
CC FT FTId=VSP_010705.
CC FT Missing (in isoform 2).
CC FT FTId=VSP_010706.
CC FT T -> I (in SNCV).
CC FT FTId=VAR_019118.
CC FT D -> V (in Ref. 3; AAH40474).
CC FT CONFLICT 270 270 Missing (in Ref. 3; AAH36809).
CC FT CONFLICT 627 627 T -> S (in Ref. 4).
CC FT CONFLICT 794 794 S -> T (in Ref. 4).
CC FT CONFLICT 816 816
CC SEQUENCE 1139 AA; 127119 MW; 8F85F21F327F0CE7 CRC64;
CC
```

```
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 136 LILKXEDE 143
Db 565 LILKXEDE 572
Search completed: January 30, 2006, 08:58:07
Job time : 171 secs
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Query Match 5.1%; Score 8; DB 1; Length 1139;  
Best Local Similarity 100.0%; Pred. No. 35;

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.  
OM protein - protein search, using sw model  
Run on: January 30, 2006, 08:59:06 ; Search time 32 Seconds  
(without alignments)  
53.130 Million cell updates/sec

Title: US-09-716-356A-6  
Perfect score: 157  
Sequence: 1 YFGKLESKLSVIRLNQDVL.....LKKEDELGDRSIMFTVQNEED 157

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 75621 seqs, 10829074 residues

Word size : 0

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 100 summaries

Database : Published Applications AA New:  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	53.5	157	6	US-10-401-386B-64
2	84	53.5	157	6	US-10-401-386B-70
3	84	53.5	157	6	US-10-401-386B-76
4	84	53.5	157	6	US-10-401-386B-78
5	84	53.5	157	6	US-10-401-386B-80
6	81	51.6	157	6	US-10-401-386B-68
7	55	35.0	157	6	US-10-401-386B-66
8	54	34.4	157	6	US-10-401-386B-72
9	54	5.1	556	7	US-11-024-959-470
10	7	4.5	366	7	US-11-024-959-470
11	6	3.8	16	7	US-11-106-932-56
12	6	3.8	31	7	US-11-106-932-4
13	6	3.8	151	6	US-10-793-626-2696
14	6	3.8	199	7	US-11-113-424-44
15	6	3.8	209	7	US-11-055-822-88
16	6	3.8	209	7	US-11-055-822-90
17	6	3.8	256	6	US-10-877-346-74
18	6	3.8	281	6	US-10-131-826A-372
19	6	3.8	310	6	US-10-063-703-140
20	6	3.8	310	7	US-11-102-240-140
21	6	3.8	318	7	US-11-109-156-15
22	6	3.8	318	7	US-11-111-239-2
23	6	3.8	333	7	US-11-004-789-2
24	6	3.8	334	7	US-11-111-239-4
25	6	3.8	334	7	US-11-127-817-14
26	6	3.8	334	7	US-11-127-877-69
27	6	3.8	338	7	US-11-151-601-18
28	6	3.8	344	6	US-10-467-657-2616
29	6	3.8	344	6	US-10-995-561-740
30	6	3.8	344	6	US-10-995-561-744
31	6	3.8	389	6	US-10-821-234-1401
32	6	3.8	391	6	US-10-995-561-739
33	6	3.8	409	6	US-10-517-939-292
34	6	3.8	432	6	US-10-995-561-738
35	6	3.8	436	6	US-10-131-826A-404
36	6	3.8	445	6	US-10-995-561-746
37	6	3.8	452	6	US-10-793-626-1834
38	6	3.8	457	6	US-10-995-561-741
39	6	3.8	491	6	US-10-995-561-743
40	6	3.8	512	6	US-10-995-561-745
41	6	3.8	615	7	US-11-172-145-6
42	6	3.8	617	7	US-11-172-145-8
43	6	3.8	651	7	US-11-172-145-10
44	6	3.8	655	6	US-10-467-657-3168
45	6	3.8	753	6	US-10-485-517-173
46	6	3.8	1094	6	US-10-517-939-144
47	6	3.8	1104	7	US-11-099-855-11
48	6	3.8	1198	6	US-10-453-372-880
49	6	3.8	1450	6	US-10-055-877-48
50	6	3.8	1450	6	US-10-453-372-874
51	6	3.8	2551	7	US-11-052-554A-368
52	6	3.8	3568	6	US-10-453-372-194
53	6	3.8	3570	6	US-10-453-372-178
54	6	3.8	3570	6	US-10-453-372-196
55	6	3.8	3570	6	US-10-453-372-198
56	6	3.8	3570	6	US-10-453-372-200
57	6	3.8	3570	6	US-10-453-372-202
58	6	3.8	3570	6	US-10-453-372-204
59	6	3.8	3570	6	US-10-453-372-206
60	5	3.2	8	7	US-11-045-024-2504
61	5	3.2	8	7	US-11-045-024-2504
62	5	3.2	9	7	US-11-045-024-2516
63	5	3.2	10	6	US-10-880-238-30
64	5	3.2	10	6	US-10-880-238-33
65	5	3.2	13	6	US-10-509-917-3
66	5	3.2	15	6	US-10-889-197-9
67	5	3.2	15	7	US-11-022-562-22
68	5	3.2	15	7	US-11-022-562-23
69	5	3.2	17	6	US-10-989-226-2
70	5	3.2	17	6	US-10-834-397-233
71	5	3.2	17	7	US-11-066-967-29
72	5	3.2	17	6	US-10-929-988-338
73	5	3.2	18	6	US-10-889-197-13
74	5	3.2	18	6	US-10-929-988-339
75	5	3.2	18	6	US-10-929-988-340
76	5	3.2	18	6	US-10-929-988-475
77	5	3.2	18	7	US-11-033-039-998
78	5	3.2	20	7	US-11-022-562-276
79	5	3.2	20	7	US-11-022-562-277
80	5	3.2	20	7	US-11-022-562-278
81	5	3.2	20	7	US-11-022-562-279
82	5	3.2	20	7	US-11-041-893-190
83	5	3.2	22	7	US-11-041-893-197
84	5	3.2	23	7	US-11-041-893-195
85	5	3.2	27	7	US-11-031-851-5
86	5	3.2	27	7	US-11-031-851-7
87	5	3.2	27	7	US-11-031-851-19
88	5	3.2	27	7	US-11-031-851-21
89	5	3.2	28	7	US-11-031-851-11
90	5	3.2	28	7	US-11-031-851-20
91	5	3.2	29	7	US-11-031-851-12
92	5	3.2	29	7	US-11-031-851-13
93	5	3.2	29	7	US-11-031-851-14
94	5	3.2	29	7	US-11-031-851-15
95	5	3.2	29	7	US-11-031-851-23
96	5	3.2	30	6	US-10-467-657-2370
97	5	3.2	37	6	US-10-957-351-24
98	5	3.2	37	6	US-10-957-351-139

99 5 3.2 43 6 US-10-957-887B-230 Sequence 230, App  
100 5 3.2 47 6 US-10-467-657-4844 Sequence 4844, Ap

## ALIGNMENTS

RESULT 1  
US-10-401-386B-64  
; Sequence 64, Application US/10401386B  
; Publication No. US20050261213A1  
; GENERAL INFORMATION:  
; APPLICANT: Patrick Branigan  
; APPLICANT: Theresa J Goletz  
; APPLICANT: David M Knight  
; APPLICANT: Stephen G McCarthy  
; APPLICANT: Bernard J Scallion  
; APPLICANT: Linda A Snyder  
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods  
; FILE REFERENCE: for Use  
; FILE REFERENCE: CEN 310CIP  
; CURRENT APPLICATION NUMBER: US/10/401,386B  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: 10/247,203  
; PRIOR FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: 60/328,371  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 64  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-401-386B-64

Query Match 53.5%; Score 84; DB 6; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.5e-78;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNKDKTSIIFFQSVPGHDKMKQFESSSYGYFLACEKERDL 133  
Db LSCENKIISFKEMNPPDNKDKTSIIFFQSVPGHDKMKQFESSSYGYFLACEKERDL 133

QY 134 FKLLKKEDELGDRSIMFTVQNEED 157  
Db FKLLKKEDELGDRSIMFTVQNEED 157

RESULT 2  
US-10-401-386B-70  
; Sequence 70, Application US/10401386B  
; Publication No. US20050261213A1  
; GENERAL INFORMATION:  
; APPLICANT: Patrick Branigan  
; APPLICANT: Theresa J Goletz  
; APPLICANT: David M Knight  
; APPLICANT: Stephen G McCarthy  
; APPLICANT: Bernard J Scallion  
; APPLICANT: Linda A Snyder  
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods  
; FILE REFERENCE: for Use  
; FILE REFERENCE: CEN 310CIP  
; CURRENT APPLICATION NUMBER: US/10/401,386B  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: 10/247,203  
; PRIOR FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: 60/328,371  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 70  
; LENGTH: 157  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-10-401-386B-70

Query Match 53.5%; Score 84; DB 6; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.5e-78;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNKDKTSIIFFQSVPGHDKMKQFESSSYGYFLACEKERDL 133  
Db LSCENKIISFKEMNPPDNKDKTSIIFFQSVPGHDKMKQFESSSYGYFLACEKERDL 133  
QY 134 FKLLKKEDELGDRSIMFTVQNEED 157  
Db FKLLKKEDELGDRSIMFTVQNEED 157

RESULT 3  
US-10-401-386B-76  
; Sequence 76, Application US/10401386B  
; Publication No. US20050261213A1  
; GENERAL INFORMATION:  
; APPLICANT: Patrick Branigan  
; APPLICANT: Theresa J Goletz  
; APPLICANT: David M Knight  
; APPLICANT: Stephen G McCarthy  
; APPLICANT: Bernard J Scallion  
; APPLICANT: Linda A Snyder  
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods  
; FILE REFERENCE: for Use  
; FILE REFERENCE: CEN 310CIP  
; CURRENT APPLICATION NUMBER: US/10/401,386B  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: 10/247,203  
; PRIOR FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: 60/328,371  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 76  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-401-386B-76

Query Match 53.5%; Score 84; DB 6; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.5e-78;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNKDKTSIIFFQSVPGHDKMKQFESSSYGYFLACEKERDL 133  
Db LSCENKIISFKEMNPPDNKDKTSIIFFQSVPGHDKMKQFESSSYGYFLACEKERDL 133  
QY 134 FKLLKKEDELGDRSIMFTVQNEED 157  
Db FKLLKKEDELGDRSIMFTVQNEED 157

RESULT 4  
US-10-401-386B-78  
; Sequence 78, Application US/10401386B  
; Publication No. US20050261213A1  
; GENERAL INFORMATION:  
; APPLICANT: Patrick Branigan  
; APPLICANT: Theresa J Goletz  
; APPLICANT: David M Knight  
; APPLICANT: Stephen G McCarthy  
; APPLICANT: Bernard J Scallion  
; APPLICANT: Linda A Snyder  
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods  
; FILE REFERENCE: for Use  
; FILE REFERENCE: CEN 310CIP  
; CURRENT APPLICATION NUMBER: US/10/401,386B  
; CURRENT FILING DATE: 2003-03-28

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; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-78

Query Match
Best Local Similarity 53.5%; Score 84; DB 6; Length 157;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDKMQFESSSYEGYFLACEKERDL 133
Db 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDKMQFESSSYEGYFLACEKERDL 133

Qy 134 FKLIKKKEDELGDRSIMFTVQNE 157
Db 134 FKLIKKKEDELGDRSIMFTVQNE 157

RESULT 5
US-10-401-386B-80
; Sequence 80, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; TITLE OF INVENTION: for Use
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-80

Query Match
Best Local Similarity 53.5%; Score 84; DB 6; Length 157;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDKMQFESSSYEGYFLACEKERDL 133
Db 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDKMQFESSSYEGYFLACEKERDL 133

Qy 134 FKLIKKKEDELGDRSIMFTVQNE 157
Db 134 FKLIKKKEDELGDRSIMFTVQNE 157

RESULT 6
US-10-401-386B-68
; Sequence 68, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
```

```
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; TITLE OF INVENTION: for Use
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-68

Query Match
Best Local Similarity 51.6%; Score 81; DB 6; Length 157;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDKMQFESSSYEGYFLACEKERDL 133
Db 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDKMQFESSSYEGYFLACEKERDL 133

Qy 134 FKLIKKKEDELGDRSIMFTVQ 154
Db 134 FKLIKKKEDELGDRSIMFTVQ 154

RESULT 7
US-10-401-386B-66
; Sequence 66, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; TITLE OF INVENTION: for Use
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-66

Query Match
Best Local Similarity 35.0%; Score 55; DB 6; Length 157;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 QVLFIDQGNRPLFEDMTDSDCRNAPRTFIISMYKDSOPRGMAVTISVKCEKIS 72
Db 18 QVLFIDQGNRPLFEDMTDSDCRNAPRTFIISMYKDSOPRGMAVTISVKCEKIS 72

RESULT 8
US-10-401-386B-72
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; Sequence 72, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Brangan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: CEN 310C1P
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-10-401-386B-72

Query Match      34.4%; Score 54; DB 6; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.2e-48;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 IISFKEMNPPDNIKDKTSIIIFQRSVPGHDNKKQFESSYEGYFLACEKERDL 133
DB 80 IISFKEMNPPDNIKDKTSIIIFQRSVPGHDNKKQFESSYEGYFLACEKERDL 133

RESULT 9
US-11-124-368A-303
; Sequence 303, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-303

Query Match      5.1%; Score 8; DB 7; Length 556;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 ILKKEDEL 144
DB 428 ILKKEDEL 435

RESULT 10
US-11-024-959-470
; Sequence 470, Application US/11024959
; Publication No. US20060010516A1
```

```
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: EMERSON, SARAH JANE
; APPLICANT: GRIGOR, MURRAY ROBERT
; APPLICANT: HIGGINS, COLLEEN M.
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: KODRZYCKI, BOB
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
; FILE REFERENCE: 044463-0360
; CURRENT APPLICATION NUMBER: US/11/024,959
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/533,036
; PRIOR FILING DATE: 2003-12-30
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 470
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Pinus radiata
US-11-024-959-470

Query Match      4.5%; Score 7; DB 7; Length 366;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 KLILKE 141
DB 316 KLILKE 322

RESULT 11
US-11-106-932-56
; Sequence 56, Application US/11106932
; Publication No. US20050260697A1
; GENERAL INFORMATION:
; APPLICANT: WANG, KA-WANG KEVIN
; APPLICANT: HAYES, RONALD
; APPLICANT: LIU, MING CHEN
; APPLICANT: OLI, MONIKA
; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
; FILE REFERENCE: 5853-549-1
; CURRENT APPLICATION NUMBER: US/11/106,932
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-932-56

Query Match      3.8%; Score 6; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 EKERDL 133
DB 8 EKERDL 13

RESULT 12
US-11-106-932-4
; Sequence 4, Application US/11106932
; Publication No. US20050260697A1
; GENERAL INFORMATION:
; APPLICANT: WANG, KA-WANG KEVIN
; APPLICANT: HAYES, RONALD
; APPLICANT: LIU, MING CHEN
; APPLICANT: OLI, MONIKA
; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
```



```
; TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
; FILE REFERENCE: 5853-549-1
; CURRENT APPLICATION NUMBER: US/11/106,932
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-932-4

Query Match          3.8%; Score 6; DB 7; Length 31;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 EKERDL 133
DB 23 EKERDL 28
|||||

RESULT 13
US-10-793-626-2696
; Sequence 2696, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2696
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2696

Query Match          3.8%; Score 6; DB 6; Length 151;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 TIFIIS 50
DB 35 TIFIIS 40
|||||

RESULT 14
US-11-113-424-44
; Sequence 44, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
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; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-44

Query Match          3.8%; Score 6; DB 7; Length 199;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 GDRSIM 150
DB 144 GDRSIM 149
|||||

RESULT 15
US-11-055-822-88
; Sequence 88, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 88
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-88

Query Match          3.8%; Score 6; DB 7; Length 209;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 SVFGHD 110
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Db 130 SVPGHD 135  
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## RESULT 16

US-11-055-822-90  
; Sequence 90, Application US/11055822  
; Publication No. US20050260707A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS  
; FILE REFERENCE: BGI-121CPN  
; CURRENT APPLICATION NUMBER: US/11/055,822  
; CURRENT FILING DATE: 2005-02-11  
; PRIOR APPLICATION NUMBER: 09/606,740  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: 60/141,031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: 60/142,101  
; PRIOR FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: 60/148,613  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 60/187,970  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: DE 19930476.9  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19931415.2  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931418.7  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931419.5  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931420.9  
; PRIOR FILING DATE: 1999-07-08  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1158  
; SEQ ID NO 90  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-11-055-822-90

Query Match 3.8%; Score 6; DB 7; Length 209;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 SVPGHD 110  
Db 130 SVPGHD 135  
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## RESULT 17

US-10-877-346-74  
; Sequence 74, Application US/10877346  
; Publication No. US20060014153A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerlach, Valerie L  
; APPLICANT: MacDougall, John R  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Stone, David  
; APPLICANT: Gunther, Erik  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Grosse, William M  
; APPLICANT: Alsobrook II, John P  
; APPLICANT: Lepley, Denise M  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Leach, Martin D  
; APPLICANT: Shinkets, Richard A  
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-124  
; CURRENT APPLICATION NUMBER: US/10/877,346  
; CURRENT FILING DATE: 2004-06-25  
; PRIOR APPLICATION NUMBER: US/09/964,956  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/235,631  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/235,633  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/235,808  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/236,064  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/236,065  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/236,066  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/236,135  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 60/237,434  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/238,321  
; PRIOR FILING DATE: 2000-10-05  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 74  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Protein kinase  
; OTHER INFORMATION: domain Consensus Sequence  
US-10-877-346-74

Query Match 3.8%; Score 6; DB 6; Length 256;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 ESSSYE 121  
Db 149 ESSSYE 154  
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## RESULT 18

US-10-131-826A-372  
; Sequence 372, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C128  
CURRENT APPLICATION NUMBER: US/10/131,826A  
CURRENT FILING DATE: 2002-04-24  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 372  
LENGTH: 281  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-131-826A-372

Query Match 3.8%; Score 6; DB 6; Length 281;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 145 GDRSIM 150  
DB 226 GDRSIM 231  
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RESULT 19  
US-10-063-703-140  
Sequence 140, Application US/10063703  
Publication No. US20060008901A1  
GENERAL INFORMATION:  
APPLICANT: Baton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ACIDS ENCODING THE SAME  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,703  
CURRENT FILING DATE: 2002-05-08  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 140  
LENGTH: 310  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-063-703-140

Query Match 3.8%; Score 6; DB 6; Length 310;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 VIRNLN 16  
|||||

Db 133 VIRNLN 138  
RESULT 20  
US-11-102-240-140  
Sequence 140, Application US/11102240  
Publication No. US20050260647A1  
GENERAL INFORMATION:  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRES-  
SION  
FILE REFERENCE: P3230R1C106C  
CURRENT APPLICATION NUMBER: US/11/102,240  
CURRENT FILING DATE: 2005-04-08  
PRIOR APPLICATION NUMBER: 10/063662  
PRIOR FILING DATE: 2002-05-07  
PRIOR APPLICATION NUMBER: 10/006867  
PRIOR FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: 60/170262  
PRIOR FILING DATE: 199-12-09  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 140  
LENGTH: 310  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-11-102-240-140

Query Match 3.8%; Score 6; DB 7; Length 310;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 VIRNLN 16  
|||||  
Db 133 VIRNLN 138

RESULT 21  
US-11-109-156-15  
Sequence 15, Application US/11109156  
Publication No. US20050250144A1  
GENERAL INFORMATION:  
APPLICANT: Toshio Ota  
APPLICANT: Takao Isogai  
APPLICANT: Tetsuo Nishikawa  
APPLICANT: Koji Hayashi  
APPLICANT: Kaoru Otsuka  
APPLICANT: Jun-ichi Yamamoto  
APPLICANT: Shizuko Ishii  
APPLICANT: Tomoyasu Sugiyama  
APPLICANT: Ai Wakamatsu  
APPLICANT: Keiichi Nagai  
APPLICANT: Tetsuji Otsuki  
APPLICANT: Shin-ichi Funahashi  
APPLICANT: Chiaki Senoo  
APPLICANT: Jun-ichi Nezu  
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN  
PHOSPHATASE  
FILE REFERENCE: 06501-099002  
CURRENT APPLICATION NUMBER: US/11/109,156  
CURRENT FILING DATE: 2005-04-19  
PRIOR APPLICATION NUMBER: US/10/060,065  
PRIOR FILING DATE: 2002-01-29  
PRIOR APPLICATION NUMBER: PCT/JP00/05061  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: US 60/159,590  
PRIOR FILING DATE: 1999-10-18  
PRIOR APPLICATION NUMBER: US 60/183,322



;  
;  
; FILING DATE: 21-Apr-2005  
; CLASSIFICATION: <Unknown>  
;  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/761,569  
; FILING DATE: 16-Jan-2001  
; APPLICATION NUMBER: 09/057,009  
; FILING DATE: 1998-04-07  
;  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fasse, J. Peter  
; REGISTRATION NUMBER: 32,983  
; REFERENCE/DOCKET NUMBER: 07917/010001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
;  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 334 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: Not Relevant  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-11-111-239-4

Query Match 3.8%; Score 6; DB 7; Length 334;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 SKLSVI 12  
Db 171 SKLSVI 176

RESULT 25  
US-11-127-817-14  
; Sequence 14, Application US/11127817  
; Publication No. US20050287519A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions And Compound Assays For Inhibiting  
; FILE REFERENCE: P27,800-D USA  
; CURRENT APPLICATION NUMBER: US/11/127,817  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 534  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 14  
; LENGTH: 334  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-127-817-14

Query Match 3.8%; Score 6; DB 7; Length 334;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 SKLSVI 12  
Db 171 SKLSVI 176

Search completed: January 30, 2006, 09:10:33  
Job time : 32 secs

GenCore version 5.1.6  
 Copyright (c) 1993 - 2006 CompuGen Ltd.  
 OM protein - protein search, using sw model  
 Run on: January 30, 2006, 08:42:04 : Search time 134 Seconds  
 (without alignments)  
 514.795 Million cell updates/sec

Title: US-09-716-356A-6  
 Perfect score: 157  
 Sequence: 1 YFGKLESLVIRNLNDQVL.....LKKEDELGDRSIMFTVQNE 157

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0  
 Searched: 2443163 seqs, 439378781 residues

Word size : 0  
 Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : A Geneseq 21.\*  
 1: geneseqp1980s.\*  
 2: geneseqp1990s.\*  
 3: geneseqp2000s.\*  
 4: geneseqp2001s.\*  
 5: geneseqp2002s.\*  
 6: geneseqp2003as.\*  
 7: geneseqp2003bs.\*  
 8: geneseqp2004s.\*  
 9: geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	156	99.4	157	2	Aar99564 Human int
2	156	99.4	157	2	Aar99558 Human mat
3	156	99.4	157	2	Aaw15701 Interfero
4	156	99.4	157	2	Aaw24258 Human pro
5	156	99.4	157	2	Aaw63810 Human IL-
6	156	99.4	157	2	Aaw52176 Interfero
7	156	99.4	157	2	Aaw77158 Human int
8	156	99.4	157	2	Aaw37741 IFN-gamma
9	156	99.4	157	2	Aay39799 Interleuk
10	156	99.4	157	3	Aay53904 Sequence
11	156	99.4	157	3	Aay44597 Human int
12	156	99.4	157	4	Aab82408 Human int
13	156	99.4	193	2	Aar99560 Human int
14	156	99.4	193	2	AAW52172 Interfero
15	156	99.4	193	2	AAW47429 Interfero
16	156	99.4	193	2	AAW37740 Interfero
17	156	99.4	193	3	AAV53908 Amino aci
18	156	99.4	193	4	ABR82409 Human int
19	156	99.4	193	8	ADL24278 Human IL-
20	84	53.5	157	2	AAW77084 Human int
21	84	53.5	157	- 2	AAW77077 Human int
22	84	53.5	157	2	AAW77083 Human int
23	84	53.5	157	2	AAW48961 Mutant hu
24	84	53.5	157	2	AAW48962 Mutant hu

25	84	53.5	157	3	AAV57570 Human int
26	84	53.5	157	4	AAG65351 Human int
27	84	53.5	157	4	AAG65294 Human int
28	84	53.5	157	4	AAE06661 Human int
29	84	53.5	157	5	ABO4389 Human IL-
30	84	53.5	157	5	AAE17134 Human IL-
31	84	53.5	157	5	AAE16954 Human act
32	84	53.5	157	6	ABG73364 Human mat
33	84	53.5	157	6	ABG73365 Human mat
34	84	53.5	157	6	ABG73363 Human mat
35	84	53.5	157	6	ABG73367 Human mat
36	84	53.5	157	6	ABG73359 Human wil
37	84	53.5	157	6	ADA50616 Human mat
38	84	53.5	157	6	ADA50622 Human mat
39	84	53.5	157	6	ADA50610 Human mat
40	84	53.5	157	6	ABR83396 Human int
41	84	53.5	157	6	ABR83405 Human int
42	84	53.5	157	6	ABR83406 Human int
43	84	53.5	157	6	ABR83407 Human int
44	84	53.5	157	6	ABR83404 Human int
45	84	53.5	157	6	ABR83372 Human int
46	84	53.5	157	6	ABR83402 Human int
47	84	53.5	157	6	ABR83399 Human int
48	84	53.5	157	6	ABR83401 Human int
49	84	53.5	157	6	ABR83403 Human int
50	84	53.5	157	6	ABR83394 Human int
51	84	53.5	157	6	ABR83397 Human int
52	84	53.5	157	6	ABR83395 Human int
53	84	53.5	157	6	ABR83398 Human int
54	84	53.5	157	7	AAE39507 Human mat
55	84	53.5	157	7	ADG06775 Human ant
56	84	53.5	157	8	ADH54826 Human int
57	84	53.5	157	8	ADL24279 Human IL-
58	84	53.5	157	8	ADN35070 Human IL-
59	84	53.5	157	8	ADG73367 Human int
60	84	53.5	157	8	ADU06896 Human int
61	84	53.5	157	8	ADU06893 Human int
62	84	53.5	157	8	ADU06897 Human int
63	84	53.5	157	8	ADU49648 Human int
64	84	53.5	157	8	ADU49654 Human IL-
65	84	53.5	157	8	ADU49658 Human IL-
66	84	53.5	157	8	ADU49642 Human int
67	84	53.5	157	8	ADU49656 Human IL-
68	84	53.5	157	9	ADV90268 Protease-
69	84	53.5	157	9	ADY86605 Human rec
70	84	53.5	157	9	ADZ77759 Human int
71	84	53.5	157	9	ADZ77756 Human int
72	84	53.5	157	9	AEb93714 Human mut
73	84	53.5	157	9	AEb93702 Human wil
74	84	53.5	158	3	AAV85167 Human int
75	84	53.5	158	8	ADJ88309 Human int
76	84	53.5	158	8	ADO04682 Human int
77	84	53.5	177	6	ADA50614 Mature co
78	84	53.5	180	2	AAW48959 Wild-type
79	84	53.5	181	3	AAZ23797 Human int
80	84	53.5	193	2	AAW22047 Interfero
81	84	53.5	193	2	AAW46592 Amino aci
82	84	53.5	193	4	AAAB30541 A human I
83	84	53.5	193	4	AAAG63830 Amino aci
84	84	53.5	193	5	AAE16953 Human pre
85	84	53.5	193	6	ABG73366 Human pre
86	84	53.5	193	6	ABG73360 Human pre
87	84	53.5	193	6	ABG73361 Human pre
88	84	53.5	193	6	ABG73362 Human pre
89	84	53.5	193	7	AAE39505 Human aci
90	84	53.5	193	8	ADN41835 Amino aci
91	84	53.5	193	8	ADP12432 Protein e
92	84	53.5	193	8	ADP64786 Human int
93	84	53.5	193	9	ADZ51271 Amino aci
94	84	53.5	193	9	ADZ70835 Human int
95	84	53.5	193	9	AEb28907 Human int
96	84	53.5	203	8	ADU06895 Human int
97	84	53.5	233	5	AAE16959 Ubiquitin

98 84 53.5 325 9 ADY22168 Human IL-  
 99 84 53.5 325 9 ADY22167 Human IL-  
 100 84 53.5 361 9 ADY22165 Human IL-

## ALIGNMENTS

RESULT 1  
 AAR99564  
 ID AAR99564 standard; protein; 157 AA.  
 XX  
 AC AAR99564;  
 XX  
 DT 29-SEP-1996 (first entry)  
 XX  
 DE Human interferon-gamma inducer protein.  
 XX  
 KW Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;  
 KW antitumour; antibacterial; immunoregulator; adoptive immunotherapy;  
 KW therapy; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 73  
 FT /label= Ile, Thr  
 XX  
 PN EP712931-A2.  
 XX  
 PD 22-MAY-1996.  
 XX  
 PF 10-NOV-1995; 95EP-00308055.  
 XX  
 PR 15-NOV-1994; 94JP-00304203.  
 PR 23-FEB-1995; 95JP-00058240.  
 PR 10-MAR-1995; 95JP-00078357.  
 PR 18-SEP-1995; 95JP-00262062.  
 PR 29-SEP-1995; 95JP-00274988.  
 XX  
 PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
 XX  
 PI Ushio S, Torigoe K, Tanimoto T, Okamura H, Kunikata T;  
 PI Taniguchi M, Kohno K, Fukuda S, Kurimoto M;  
 XX  
 DR WPI; 1996-252837/26.  
 DR N-PSDB; AAT32411.  
 XX  
 PT DNA encoding interferon-gamma prodn.-inducing polypeptide - useful to  
 PT treat and prevent, e.g. viral disease, malignancies and immune disorders.  
 XX  
 PS Example B-1-1; Page 28; 48pp; English.  
 XX  
 CC A novel human protein (AAR99564) that induces interferon-gamma (IFN-  
 CC gamma) prodn. by immunocompetent cells is the product of a phage cDNA  
 CC clone (AAT32411) derived from a human liver library. PCR amplification of  
 CC the cDNA (see also AAT32409-10) and expression in Escherichia coli XL-1  
 CC Blue MRF-Kan allowed prodn. of recombinant inducer protein. This was used  
 CC to construct hybridoma H-1, which produced anti-IFN-gamma inducer protein  
 CC monoclonal antibody H-1mab, useful in the detection and purification of  
 CC the inducer protein (see also AAR99558)  
 XX  
 XX Sequence 157 AA;

Query Match 99.4%; Score 156; DB 2; Length 157;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-162;  
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60  
 DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60  
 QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQFESSY 120

Db 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQFESSY 120  
 QY 121 EGYFLACCKERDLFKLILKKEDELGDRSMTPTVQNE 157  
 DB 121 EGYFLACCKERDLFKLILKKEDELGDRSMTPTVQNE 157

RESULT 2  
 AAR99558  
 ID AAR99558 standard; protein; 157 AA.  
 XX  
 AC AAR99558;  
 XX  
 DT 29-SEP-1996 (first entry)  
 XX  
 DE Human mature interferon-gamma inducer protein.  
 XX  
 KW Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;  
 KW antitumour; antibacterial; immunoregulator; adoptive immunotherapy;  
 KW therapy; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 73  
 FT /label= Ile, Thr  
 XX  
 PN EP712931-A2.  
 XX  
 PD 22-MAY-1996.  
 XX  
 PF 10-NOV-1995; 95EP-00308055.  
 XX  
 PR 15-NOV-1994; 94JP-00304203.  
 PR 23-FEB-1995; 95JP-00058240.  
 PR 10-MAR-1995; 95JP-00078357.  
 PR 18-SEP-1995; 95JP-00262062.  
 PR 29-SEP-1995; 95JP-00274988.  
 XX  
 PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
 XX  
 PI Ushio S, Torigoe K, Tanimoto T, Okamura H, Kunikata T;  
 PI Taniguchi M, Kohno K, Fukuda S, Kurimoto M;  
 XX  
 DR WPI; 1996-252837/26.  
 DR N-PSDB; AAT32402.  
 XX  
 PT DNA encoding interferon-gamma prodn.-inducing polypeptide - useful to  
 PT treat and prevent, e.g. viral disease, malignancies and immune disorders.  
 XX  
 PS Claim 1; Page 40; 48pp; English.  
 XX  
 CC A novel human protein (AAR99558) induces interferon-gamma (IFN-gamma)  
 CC prodn. by immunocompetent cells. It enhances the cytotoxicity of killer  
 CC cells and/or induces the formation of killer cells (e.g. NK cells,  
 CC lymphokine-activating killer (LAK) cells, and cytotoxic T-cells).  
 CC Recombinant IFN-gamma inducer protein can be produced in high yields  
 CC using host cells, esp. Escherichia coli, transformed with a vector  
 CC carrying the encoding cDNA (AAT32402). It is useful as an antiviral,  
 CC antitumor, antibacterial, immunoregulatory and blood platelet enhancing  
 CC agent, and can be used in adoptive immunotherapy. It is also used to  
 CC raise monoclonal antibodies. A full-length sequence is given in AAR99560  
 XX  
 XX Sequence 157 AA;

Query Match 99.4%; Score 156; DB 2; Length 157;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-162;  
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60  
 DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60

QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQSRVPGHDKMKQFESSY 120  
 DB 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQSRVPGHDKMKQFESSY 120  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
 DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 3  
 AAW15701  
 ID AAW15701 standard; protein; 157 AA.  
 XX  
 AC AAW15701;  
 DT 26-JAN-1998 (first entry)  
 XX  
 DE Interferon-gamma inducer protein.  
 XX  
 KW Interferon-gamma, IFN-gamma; antiviral; antioncotic; radiotherapy;  
 KW immunoregulatory; antitumour agent; chemotherapy; leukopaemia;  
 KW thrombocytopaenia; immunocompetent cell; asthma; hayfever; rheumatism;  
 KW interleukin; killer cell.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 73  
 FT /label= Ile, Thr  
 XX  
 PN EP767178-Al.  
 XX  
 PD 09-APR-1997.  
 XX  
 XX 26-SEP-1996; 96EP-00306997.  
 XX  
 PR 26-SEP-1995; 95JP-00270725.  
 PR 29-FEB-1996; 96JP-00067434.  
 PR 20-SEP-1996; 96JP-00269105.  
 XX  
 PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
 XX  
 PI Akita K, Nukada Y, Fujii M, Tanimoto T, Kurimoto M;  
 XX  
 DR WPI; 1997-205381/19.  
 XX  
 PT Human protein that induces interferon-gamma prodn. in immuno:competent  
 PT cells - useful for adoptive immuno:therapy of tumours and as  
 PT antimicrobial agent etc.  
 XX  
 PS Claim 8; Page 20; 26pp; English.  
 XX  
 CC The present sequence represents a novel protein from human cells, which  
 CC induces interferon-gamma (IFN gamma) production in immunocompetent cells.  
 CC This protein enhances cytotoxicity of killer cells and induces their  
 CC formation. It is used as an antioncotic agent for antitumour  
 CC immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent,  
 CC and in the treatment of atopic or immune system diseases, e.g. asthma,  
 CC hayfever or rheumatism. When formulated with interleukin-3, it is also  
 CC used to treat leukopaemia and thrombocytopaenia associated with  
 CC radiotherapy or chemotherapy of leukaemia and other cancers. When used in  
 CC antitumour immunotherapy, this novel protein significantly improves the  
 CC immunotherapeutic effect of interleukin-2 (IL-2), compared with use of IL  
 CC -2 alone, either when administered to the patient (before administration  
 CC of IL-2) or by addition to the medium in which cells (intended for return  
 CC to the patient) are being grown

XX Sequence 157 AA;

Query Match 99.4%; Score 156; DB 2; Length 157;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-162;  
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIIDQGNRPLFEDMTSDCRDNAPRTIIFIISMYKDSQPRGM 60  
 DB 1 YFGKLESKLSVIRNLNDQVLFIIDQGNRPLFEDMTSDCRDNAPRTIIFIISMYKDSQPRGM 60  
 QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQSRVPGHDKMKQFESSY 120  
 DB 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQSRVPGHDKMKQFESSY 120  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
 DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 4  
 AAW24258  
 ID AAW24258 standard; protein; 157 AA.  
 XX  
 AC AAW24258;  
 XX  
 DT 15-OCT-1997 (first entry)  
 XX  
 DE Human protein for induction of interferon-gamma.  
 XX  
 KW Interferon-gamma; immunocompetent cell; malignant tumour; viral disease;  
 KW bacterial infection; immune disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 73  
 FT /note= "Encoded by AYT"  
 FT  
 PN JP09157180-A.  
 XX  
 PD 17-JUN-1997.  
 XX  
 PF 24-JAN-1996; 96JP-00028722.  
 XX  
 PR 10-MAR-1995; 95JP-00078357.  
 PR 29-SEP-1995; 95JP-00274988.  
 PR 04-OCT-1995; 95JP-00279906.  
 XX  
 PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
 XX  
 DR WPI; 1997-369391/34.  
 DR N-PSDB; AAT80209.  
 XX  
 PT A drug containing a polypeptide which induces interferon-gamma - useful  
 PT for treating e.g. malignant tumours, viral, bacterial or immune diseases.  
 XX  
 PS Claim 1; Page 9; 12pp; Japanese.  
 XX  
 CC This sequence represents a protein which induces interferon-gamma  
 CC production in immunocompetent cells. This protein may be used as the  
 CC major component in a drug for the prevention and treatment of e.g.  
 CC malignant tumours, viral diseases, bacterial infections and immune  
 CC diseases  
 XX  
 SQ Sequence 157 AA;

Query Match 99.4%; Score 156; DB 2; Length 157;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-162;  
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIIDQGNRPLFEDMTSDCRDNAPRTIIFIISMYKDSQPRGM 60  
 DB 1 YFGKLESKLSVIRNLNDQVLFIIDQGNRPLFEDMTSDCRDNAPRTIIFIISMYKDSQPRGM 60  
 QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQSRVPGHDKMKQFESSY 120  
 DB 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQSRVPGHDKMKQFESSY 120



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QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

RESULT 5
AAW63810
ID AAW63810 standard; protein; 157 AA.
AC AAW63810;
XX 28-SEP-1998 (first entry)
XX Human IL-18 protein fragment.
DE Interleukin-18: IL-18; human; treatment; autoimmune disease; antibody;
KW immunosuppressant; inhibitor; receptor protein; detection.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Protein 1..157
FT /label= IL-18
FT /note= "partial sequence"
FT Misc-difference 73
FT /label= Thr or Ile
XX EP850952-A1.
PN 01-JUL-1998.
XX 23-DEC-1997; 97EP-00310555.
XX 26-DEC-1996; 96JP-00356426.
PR 21-FEB-1997; 97JP-00052526.
PR 06-JUN-1997; 97JP-00163490.
PR 28-JUL-1997; 97JP-00215490.
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA Torigoe K, Ushio S, Kunikata T, Kurimoto M;
XX WPI; 1998-335317/30.
XX New interleukin-18 receptor protein - used to inhibit interleukin-18, to
PT treat autoimmune disease and as immunosuppressant to treat e.g. graft
PT rejection, insulin-resistant diabetes and ulcerative colitis.
XX Claim 5; Page 16; 35pp; English.
XX This sequence represents a human interleukin-18 (IL-18) fragment which is
CC used in a method involved in neutralising IL-18 or to treat autoimmune
CC diseases or as an immunosuppressant using anti-IL-18 antibodies which can
CC inhibit IL-18. Such antibodies can also be used to detect the IL-18
CC receptor protein (labelled with an enzyme or a radioactive or fluorescent
CC substance). The protein is used to treat e.g. graft rejection, pernicious
CC anaemia, atrophic gastritis, insulin-resistant diabetes, Wegener
CC granulomatosis, discoid lupus erythematosus, ulcerative colitis, cold-
CC agglutinin-relating diseases, Goodpasture's syndrome, primary biliary
CC cirrhosis, sympathetic ophthalmitis, hyperthyroidism, juvenile onset type
CC diabetes, Sjogren syndrome, autoimmune hepatitis, autoimmune haemolytic
CC anaemia, myasthenia gravis, systemic scleroderma, systemic lupus
CC erythematosus, polyplectic cold haemoglobinuria, polymyositis,
CC periarthritis nodosa, multiple sclerosis, Addison's disease, purpura
CC haemorrhagica, Basedow's disease, leukopaenia, Behcet's disease,
CC clinacarium praecox, rheumatoid arthritis, rheumatopyra, chronic
CC thyroiditis, Hodgkin's disease, HIV, asthma, atopic dermatitis, allergic
CC nasitis, pollinosis, apitoxin-allergy and septic shock resulting from
CC production or administration of excessive gamma interferon (IFN-gamma)
XX Sequence 157 AA;
Query Match 99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.le-162; Indels 0; Gaps 0;
Matches 157; Conservative 0; Mismatches 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60

RESULT 6
AAW52176
ID AAW52176 standard; peptide; 157 AA.
AC AAW52176;
XX 10-JUN-1998 (first entry)
XX Interferon-gamma inducing mature polypeptide.
DE Interferon-gamma; IFN-gamma; precursor; enzyme; cleavage.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Misc-difference 73 /label= Ile, Thr
FT EP819757-A2.
XX 21-JAN-1998.
XX 18-JUL-1997; 97EP-00305377.
XX 19-JUL-1996; 96JP-00207691.
PR 30-MAY-1997; 97JP-00156062.
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA Tanimoto T, Kurimoto M;
XX WPI; 1998-078838/08.
XX Polypeptide-processing enzyme - for preparing mature form of interferon-
PT inducing polypeptide.
XX Claim 20; Page 17; 18pp; English.
XX This is an interferon-gamma (IFN-gamma) inducing polypeptide sequence.
CC This polypeptide induces IFN-gamma production in immunocompetent cells
CC [the polypeptide is not named but is described in JP 27198/96 and
CC 193098/96]. An enzyme can convert the precursor form of this polypeptide
CC into this active form by cleaving a linkage between Asp at amino acid
CC position 36 and Tyr at amino acid position 37 of the precursor. The
CC enzyme can be obtained from a human haematopoietic cell and can be
CC inhibited by iodoacetamide and acetyl-L-tyrosyl-L-valyl-L-alanyl-L-
CC aspart-L-al. The enzyme can be used for cleaving a recombinant IFN-gamma
CC pro-polypeptide to form a mature polypeptide
XX Sequence 157 AA;
Query Match 99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.le-162; Indels 0; Gaps 0;
Matches 157; Conservative 0; Mismatches 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60
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Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQORSVPGHDNKMQFESSY 120  
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQORSVPGHDNKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

## RESULT 7

AAW77158  
ID AAW77158 standard; protein; 157 AA.

XX  
AC AAW77158;

DT 26-NOV-1998 (first entry)

XX Human interleukin-18 protein (IL-18).

DE Human; interleukin-18 receptor; IL-18R; cytokine; signal transduction;  
KW immune system; treatment; autoimmune; allergic disease;  
KW immunosuppressant.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH Misc-difference 73  
FT /note= "Ile or Thr"

XX EP864585-A1.

XX 16-SEP-1998.

XX 23-DEC-1997; 97EP-00310517.

XX 12-MAR-1997; 97JP-00074697.

XX 28-JUL-1997; 97JP-00215488.

XX 09-OCT-1997; 97JP-00291837.

XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.

XX Torigoe K, Okura T, Kurimoto M;

XX WPI; 1998-469188/41.

XX Interleukin-18 receptor polypeptide(s) - and corresponding DNA, which  
PT peptide compounds are useful for treating auto-immune or allergic  
PT diseases.

XX Disclosure; Page 41-42; 51pp; English.

XX The present sequence represents a human interleukin-18 (IL-18)  
CC polypeptide. Interleukin-18 is a type of cytokine which mediates signal  
CC transduction in immune systems. The interleukin-18 receptor polypeptide  
CC can be used to neutralise interleukin-18 activity or to treat interleukin  
CC -18 receptor susceptible diseases, especially to treat autoimmune or  
CC allergic diseases or as an immunosuppressant. Conditions which may be  
CC treated include e.g. graft or organ rejection, pernicious anaemia,  
CC insulin-related diabetes, discoid lupus erythematosus, ulcerative  
CC colitis, hyperthyroidism, auto-immune hepatitis, systemic scleroderma,  
CC polymyositis, leukopenia, rheumatoid arthritis, HIV infections, asthma,  
CC atopic dermatitis, and pollinosis. The products may also be useful in the  
CC treatment of septic shock associated with IFN-alpha

XX Sequence 157 AA;

Query Match 99.4%; Score 156; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No: 2.1e-162;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQORSVPGHDNKMQFESSY 120  
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQORSVPGHDNKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

## RESULT 8

AAW37741

ID AAW37741 standard; protein; 157 AA.

XX  
AC AAW37741;

DT 07-JUL-1998 (first entry)

XX IFN-gamma inducing active protein.

DE Interferon-gamma inducing precursor peptide; IFN-gamma;  
KW Interleukin-1-beta-converting enzyme; ICE; cytotoxicity; killer cell;  
KW antiviral agent; antitumour agent; immunopathy agent; antiseptic.

XX Mammalia.

XX Key Location/Qualifiers  
FH Misc-difference 73  
FT /label= Ile, Thr

XX EP821005-A2.

XX 28-JAN-1998.

XX 18-JUL-1997; 97EP-00305376.

XX 25-JUL-1996; 96JP-00213267.

XX 31-JAN-1997; 97JP-00031474.

XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.

XX Tanimoto T, Kurimoto M;

XX WPI; 1998-088847/09.

XX N-PSDB; AAV18906.

XX Conversion of interferon-inducing polypeptide precursor to active  
PT polypeptide - comprises use of interferon-1-beta-converting enzyme,  
PT useful for, e.g. enhancing cytotoxicity by killer cells.

XX Claim 5; Page 15; 18pp; English.

XX This is the amino acid sequence for the interferon-gamma (IFN-gamma)  
CC inducing active protein which is cleaved to form the active mature  
CC protein when it is in contact with interleukin-1-beta-converting enzyme  
CC (ICE). The polypeptide is used for inducing, e.g. production of IFN-gamma  
CC a useful biologically active substance, enhancing cytotoxicity by, and  
CC inducing the formation of killer cells. The polypeptide may potentially  
CC be used as an antiviral, antitumour and immunopathy agent and as an  
CC antiseptic

XX Sequence 157 AA;

Query Match 99.4%; Score 156; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No: 2.1e-162;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

```
QY 61 AVTISVCKEKLXSLSCENKIISFKEMNPPDNIKDTSKDIIFQFORSVPGHDKMKQFESSY 120
Db 61 AVTISVCKEKLXSLSCENKIISFKEMNPPDNIKDTSKDIIFQFORSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTQVNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTQVNE 157

RESULT 9
AAY39799
ID AAY39799 standard; protein; 157 AA.
XX
AC AAY39799;
XX
DT 29-NOV-1999 (first entry)
XX
DE Interleukin-18 receptor protein sequence fragment.
XX
KW Interleukin-18 receptor; IL-18; human; mouse; organ transplant rejection;
KW IL-18 receptor sensitive disease; immune reaction; therapy.
XX
OS Mammalia.
XX
FH Key Location/Qualifiers
FT Misc-difference 73
FT /note= "unspecified amino acid"
XX
PN JP11240898-A.
PD 07-SEP-1999.
XX
PF 12-MAR-1998; 98JP-00078549.
XX
PR 12-MAR-1997; 97JP-00074697.
PR 28-JUL-1997; 97JP-00215488.
PR 09-OCT-1997; 97JP-00291837.
PR 28-DEC-1997; 97JP-00366908.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX WPI; 1999-555071/47.
XX
PT New polypeptide - useful against interleukin-18 receptor sensitive
PT diseases.
XX
PS Disclosure; Page 37; 41pp; Japanese.
XX
CC This sequence is a fragment of an interleukin-18 receptor (IL-18R) of the
CC invention. The IL-18R sequences were isolated from human and mouse. The
CC sequences can be used in drugs for treating IL-18 receptor sensitive
CC disease, especially effective for the relief of rejection accompanied to
CC organ transplantation and for the treatment and the prevention of various
CC diseases caused by excessive immune reaction.
XX
SQ Sequence 157 AA;
Query Match 99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.1e-162;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPKLSEKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRNAPRTPIIISMYKDSQPRGM 60
Db 1 YFKLSEKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRNAPRTPIIISMYKDSQPRGM 60

QY 61 AVTISVCKEKLXSLSCENKIISFKEMNPPDNIKDTSKDIIFQFORSVPGHDKMKQFESSY 120
Db 61 AVTISVCKEKLXSLSCENKIISFKEMNPPDNIKDTSKDIIFQFORSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTQVNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTQVNE 157
```

```
RESULT 10
AAY53904
ID AAY53904 standard; protein; 157 AA.
XX
AC AAY53904;
XX
DT 13-MAR-2000 (first entry)
XX
DE Sequence of a mature protein that induces IFN-gamma production.
XX
KW Human; interferon gamma production; IFN-gamma; immunocompetent cell;
KW antiviral; immunoregulatory; antigen; mitogen;
KW IFN-gamma susceptible disease; antibacterial; antitumour;
KW blood platelet enhancing agent; hepatitis; herpes syndrome; condyloma;
KW AIDS; bacterial disease; Candidiasis; malaria; solid malignant tumour;
KW renal cancer; mycosis fungoides; chronic granulomatous disease;
KW blood cell malignant tumour; adult T cell leukaemia;
KW chronic myelogenous leukaemia; malignant leukaemia; immune disease;
KW allergy; rheumatism.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 73
FT /label= Ile, Thr
FT /note= "encoded by AYT"
XX
PN EP962531-A2.
PD 08-DEC-1999.
XX
PF 10-NOV-1995; 99EP-00104104.
XX
PR 15-NOV-1994; 94JP-00304203.
PR 23-FEB-1995; 95JP-00058240.
PR 10-MAR-1995; 95JP-00078357.
PR 18-SEP-1995; 95JP-00262062.
PR 29-SEP-1995; 95JP-00274988.
PR 10-NOV-1995; 95EP-00308055.
XX
PA (HAYB.) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Ushio S. Torigoe K. Tanimoto T. Okamura H.;
XX WPI; 2000-064289/06.
XX
DR N-P8DB; AA236875.
XX
PT Novel polypeptides used in the treatment of interferon-gamma susceptible
PT diseases.
XX
PS Claim 1; Page 4; 42pp; English.
XX
CC The present sequence represents a human protein that induces interferon
CC (IFN)-gamma production by immunocompetent cells. IFN-gamma is a protein
CC which has antiviral, antioncotic and immunoregulatory activities, and is
CC produced by immunocompetent cells stimulated with antigens or mitogens.
CC The protein of the invention is used to treat IFN-gamma susceptible
CC diseases, and also have use as a antiviral agent, antibacterial agent,
CC antitumour agent, immunoregulatory agent and blood platelet enhancing
CC agent. Diseases which can be treated with the protein include viral
CC diseases such as hepatitis, herpes syndrome, condyloma, and AIDS;
CC bacterial diseases such as Candidiasis and malaria; solid malignant
CC tumours such as renal cancer, mycosis fungoides, and chronic
CC granulomatous disease; blood cell malignant tumours such as adult T cell
CC leukaemia, chronic myelogenous leukaemia, and malignant leukaemia; and
CC immune diseases such as allergy and rheumatism
XX
SQ Sequence 157 AA;
Query Match 99.4%; Score 156; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.1e-162;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```





```
QY 1 YFGKLESKLSVIRNLNDVLFIDQGNRPFLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60
Db 37 YFGKLESKLSVIRNLNDVLFIDQGNRPFLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 96
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSIIFFQRSVPGHDKMQPESSSY 120
Db 97 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSIIFFQRSVPGHDKMQPESSSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 15
AAW47429
ID AAW47429 standard; protein; 193 AA.
AC AAW47429;
XX
DT 05-JUN-1998 (first entry)
XX
DE Interferon-gamma production inducer.
XX
KW Interferon-gamma; IFN-gamma; production inducer; gene therapy;
KW immunocompetent cell; treatment; prevention; malignant tumour;
KW viral infection; bacterial infection; immune disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..36
FT Peptide /label= sig_peptide
FT Peptide 37..193
FT Misc-difference 109 /label= mat_peptide
FT /label= Ile, Thr
XX
PN EP816499-A2.
XX
XX 07-JAN-1998.
XX
XX 27-JUN-1997; 97EP-00304616.
XX
XX 27-JUN-1996; 96JP-00185305.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Okura T, Torigoe K, Kurimoto M;
XX
XX WPI; 1998-054914/06.
XX
DR N-PSDB; AAV15825, AAV15826.
XX
XX GenomIT DNA encoding polypeptide inducing interferon-gamma production -
XX by immuno-competent cells, useful to treat e.g. human malignant tumours
XX or viral diseases.
XX
PS Claim 2; Page 49-50; 74pp; English.
XX
XX The present sequence is a protein, which induces interferon-gamma (IFN-
XX gamma) production in immunocompetent cells. The protein has high
XX biological activity, including enhancing cytotoxicity of killer cells and
XX inducing killer cell formation, in addition to inducing IFN-gamma.
XX production by immunocompetent cells when expressed in mammalian cells,
XX facilitating its use in low dosages to treat/prevent, e.g. malignant
XX tumours, viral or bacterial infections and immune diseases. As it is
XX expressed in mammalian cells, it also has low toxicity when used in human
XX treatments, minimising side effects. The DNA encoding the protein can be
XX used in gene therapy, e.g. by injecting vectors containing the DNA or
XX transplanting cells
XX
XX Sequence 193 AA;
```

```
Query Match 99.4%; Score 156; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.5e-162;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDVLFIDQGNRPFLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60
Db 37 YFGKLESKLSVIRNLNDVLFIDQGNRPFLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 96
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSIIFFQRSVPGHDKMQPESSSY 120
Db 97 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSIIFFQRSVPGHDKMQPESSSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 16
AAW37740
ID AAW37740 standard; protein; 193 AA.
XX
AC AAW37740;
XX
DT 07-JUL-1998 (first entry)
XX
DE Interferon-gamma inducing precursor peptide.
XX
KW Interferon-gamma inducing precursor peptide; IFN-gamma;
KW Interleukin-1-beta-converting enzyme; ICE; cytotoxicity; killer cell;
KW antiviral agent; antitumour agent; immunopathy agent; antiseptic.
XX
OS Mammalia.
XX
FH Key Location/Qualifiers
FT Protein 36..157
FT /notes= "Mature protein"
FT Cleavage-site 36..37
FT Misc-difference 109
FT /label= Ile, Thr
XX
PN EP821005-A2.
XX
XX 28-JAN-1998.
XX
XX 18-JUL-1997; 97EP-00305376.
XX
XX 25-JUL-1996; 96JP-00213267.
XX
XX 31-JAN-1997; 97JP-00031474.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Tanimoto T, Kurimoto M;
XX
XX WPI; 1998-088847/09.
XX
XX N-PSDB; AAV18906.
XX
XX Conversion of interferon-inducing polypeptide precursor to active
XX polypeptide - comprises use of interferon-1-beta-converting enzyme,
XX useful for, e.g. enhancing cytotoxicity by killer cells.
XX
XX Claim 2; Page 14-15; 18pp; English.
XX
XX This is the amino acid sequence for the interferon-gamma (IFN-gamma)
XX inducing precursor peptide, which is cleaved to form the active mature
XX protein when it is in contact with interleukin-1-beta-converting enzyme
XX (ICE). The polypeptide is used for inducing, e.g. production of IFN-gamma
XX a useful biologically active substance, enhancing cytotoxicity by, and
XX inducing the formation of killer cells. The polypeptide may potentially
XX be used as an antiviral, antitumour and immunopathy agent and as an
XX antiseptic
XX
XX Sequence 193 AA;
```

```
Query Match      99.4%; Score 156; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.5e-162;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 96

QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQORSVPGHNDKMQFESSY 120
DB 97 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQORSVPGHNDKMQFESSY 156

QY 121 EGYFLACEKERDLFKLILKKEDELGRSIMFTVQNE 157
DB 157 EGYFLACEKERDLFKLILKKEDELGRSIMFTVQNE 193

RESULT 17
AAY53908
ID AAY53908 standard; protein; 193 AA.
XX
XX AAY53908;
XX
XX 13-MAR-2000 (first entry)
XX
DE Amino acid sequence of a protein that induces IFN-gamma production.
XX
XX Human; interferon gamma production; IFN-gamma; immunocompetent cell;
XX antiviral; immunoregulatory; antigen; mitogen;
XX IFN-gamma susceptible disease; antibacterial; antitumour;
XX blood platelet enhancing agent; hepatitis; herpes syndrome; condyloma;
XX AIDS; bacterial disease; Candidiasis; malaria; solid malignant tumour;
XX renal cancer; mycosis fungoides; chronic granulomatous disease;
XX blood cell malignant tumour; adult T cell leukaemia;
XX chronic myelogenous leukaemia; malignant leukaemia;
XX immune disease allergy; rheumatism.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..36 /note= "signal peptide"
FT Protein 37..193 /note= "mature protein"
FT Misc-difference 109 /label= Ile, Thr
FT /note= "encoded by AYT"
XX
XX EP962531-A2.
XX
XX 08-DEC-1999.
XX
XX 10-NOV-1995; 99EP-00104104.
XX
XX 15-NOV-1994; 94JP-00304203.
XX 23-FEB-1995; 95JP-00058240.
XX 10-MAR-1995; 95JP-00078357.
XX 18-SEP-1995; 95JP-00262062.
XX 29-SEP-1995; 95JP-00274988.
XX 10-NOV-1995; 95EP-00308055.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA
XX Ushio S, Torigoe K, Tanimoto T, Okamura H;
PI
XX WPI; 2000-064289/06.
DR N-PSDB; AA236876.
XX
XX Novel polypeptides used in the treatment of interferon-gamma susceptible
FT diseases.
XX
XX Example A-4-3; Page 7; 42pp; English.
PS
XX
```

```
CC The present sequence represents a human protein that induces interferon
CC (IFN)-gamma production by immunocompetent cells. IFN-gamma is a protein
CC which has antiviral, antitumor and immunoregulatory activities, and is
CC produced by immunocompetent cells stimulated with antigens or mitogens.
CC The protein of the invention is used to treat IFN-gamma susceptible
CC diseases, and also have use as a antiviral agent, antibacterial agent,
CC antitumor agent, immunoregulatory agent and blood platelet enhancing
CC agent. Diseases which can be treated with the protein include viral
CC diseases such as hepatitis, herpes syndrome, condyloma, and AIDS;
CC bacterial diseases such as Candidiasis and malaria; solid malignant
CC tumours such as renal cancer, mycosis fungoides, and chronic
CC granulomatous disease; blood cell malignant tumours such as adult T cell
CC leukaemia, chronic myelogenous leukaemia, and malignant leukaemia; and
CC immune diseases such as allergy and rheumatism
XX
XX Sequence 193 AA;

Query Match      99.4%; Score 156; DB 3; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.5e-162;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 96

QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQORSVPGHNDKMQFESSY 120
DB 97 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQORSVPGHNDKMQFESSY 156

QY 121 EGYFLACEKERDLFKLILKKEDELGRSIMFTVQNE 157
DB 157 EGYFLACEKERDLFKLILKKEDELGRSIMFTVQNE 193

RESULT 18
AAB82409
ID AAB82409 standard; protein; 193 AA.
XX
XX AAB82409;
XX
XX 06-AUG-2001 (first entry)
XX
XX Human interleukin-18 precursor.
XX
XX Interleukin-18; antibody; human; infection; tumour; sarcoma;
XX autoimmune disease; therapy; diagnosis; detoxification.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..36 /label= Signal_peptide
FT Protein 37..193 /label= Mature_protein
FT Misc-difference 109 /label= Ile, Thr
XX
XX EP1101772-Al.
XX
XX 23-MAY-2001.
XX
XX 15-NOV-2000; 2000EP-00310121.
XX
XX 16-NOV-1999; 99JP-00324860.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA
XX Tohru K, Taniguchi M, Yamauchi H, Kurimoto M;
PI
XX WPI; 2001-368892/39.
DR N-PSDB; AAF90444.
XX
XX New antibodies specific to interleukin 18 (IL-18) precursor, useful in
PT
```

PT manufacturing a medicament for treating IL-18-related diseases, e.g.  
PT autoimmune disease, or for detecting, eliminating or detoxifying the  
PT precursor.

XX Example 1-2; Page 14-15; 27pp; English.

XX The present sequence is that of human interleukin-18 (IL-18) precursor.  
CC Monoclonal and polyclonal antibodies specific to the human IL-18  
CC precursor peptide (see AB82406) are claimed. These are useful in  
CC detection and purification of IL-18 precursor, and in the elimination and  
CC detoxification of the precursor accumulated in vivo. Detection methods  
CC using the antibody are effective in qualitative and quantitative analyses  
CC for the precursor, and also in the correction of imprecise results  
CC obtained from assays using anti-IL-18 antibody, which exhibit cross-  
CC reactivity against the precursor. Pharmaceutical compositions comprising  
CC an antibody specific to the IL-18 precursor can be used to treat viral  
CC infections including AIDS, bacterial infections, solid malignant tumours,  
CC malignant tumours of haemocytes, sarcomas, autoimmune disease,  
CC hepatopathy, pancreatopathy, and diseases of the gallbladder, kidney and  
CC nervous system. Detection methods using the antibody can be used to  
CC diagnose such diseases.

XX Sequence 193 AA;

Query Match 99.4%; Score 156; DB 4; Length 193;  
Best Local Similarity 100.0%; Pred. No. 2.5e-162;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 96  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKTKSDIIFQRSVPGHDKMQPESSEY 120  
DB 97 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKTKSDIIFQRSVPGHDKMQPESSEY 156  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 19

ADL24278  
ID ADL24278 standard; protein; 193 AA.  
XX  
AC ADL24278;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human IL-18.  
XX  
KW cardiovascular disease; IL-17; interleukin; IL-18; 4-1BB; CD30; OX40;  
KW antagonist.  
XX  
OS Homo sapiens.  
XX  
FN WO2004019866-A2.  
XX  
PD 11-MAR-2004.  
XX  
PP 21-AUG-2003; 2003WO-US026354.  
XX  
PR 28-AUG-2002; 2002US-0406418P.  
PR 12-AUG-2003; 2003US-0494457P.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Burton PB, Deisher TA;  
XX  
DR WPI; 2004-239107/22.  
DR N-PSDB; ADL24277.  
XX  
PT Use of IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists, for treating a

PT cardiovascular disease, e.g. chronic immune myocarditis, congestive heart  
PT failure, aneurysm, angina, embolism, restenosis, ischemia or  
PT thrombocytopenic purpura.

XX Disclosure; Page 111-112; 135pp; English.

XX The present invention relates to a method of treating cardiovascular  
CC disease in a subject, comprising administering an IL-17, IL-18, 4-1BB,  
CC CD30 or OX40 antagonist. The IL-17, IL-18, 4-1BB, CD30 or OX40  
CC antagonists are useful for treating cardiovascular disorders, e.g.  
CC (chronic immune) myocarditis, congestive heart failure, aneurysms,  
CC angina, embolism, restenosis, ischaemia or thrombocytopenic purpura. The  
CC present sequence is a polypeptide used in the exemplification of the  
CC invention.

XX Sequence 193 AA;

Query Match 99.4%; Score 156; DB 8; Length 193;  
Best Local Similarity 100.0%; Pred. No. 2.5e-162;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 96  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKTKSDIIFQRSVPGHDKMQPESSEY 120  
DB 97 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKTKSDIIFQRSVPGHDKMQPESSEY 156  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 20

AAW77084  
ID AAW77084 standard; peptide; 157 AA.  
XX  
AC AAW77084;  
XX  
DT 16-NOV-1998 (first entry)  
XX  
DE Human interleukin 18 derivative 2.  
XX  
KW Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;  
KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;  
KW chronic rheumatoid arthritis; deformity otitis; primary hyperthyroidism.  
XX  
OS Homo sapiens.  
XX  
FN EP861663-A2.  
XX  
PD 02-SEP-1998.  
XX  
PP 24-FEB-1998; 98EP-00301352.  
XX  
PR 25-FEB-1997; 97JP-00055468.  
XX  
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
XX  
PI Gillespie MT, Horwood NJ, Udagawa N, Kurimoto M;  
XX  
DR WPI; 1998-448964/39.  
XX  
PT Use of interleukin-18 to inhibit osteoclast formation - in treatment of  
PT e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome, osteosarcoma,  
PT chronic rheumatoid arthritis, deformity otitis, primary hyperthyroidism  
PT and osteoporosis.  
XX  
PS Disclosure; Page 30-31; 56pp; English.  
XX  
CC Interleukin-18 (IL-18) or a functional equivalent can be used for  
CC inhibition of osteoclast formation. IL-18 is used for treating or



CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma  
CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid  
CC arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and  
CC osteoporosis  
XX  
SQ Sequence 157 AA;

Query Match 53.5%; Score 84; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.9e-83;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKMQFESSSYEGYFLACEKERDL 133

Db 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKMQFESSSYEGYFLACEKERDL 133

QY 134 FKLILKKEDELGDRSIMFTVQNE 157

Db 134 FKLILKKEDELGDRSIMFTVQNE 157

## RESULT 21

AAW77077  
ID AAW77077 standard; peptide; 157 AA.

XX

AC AAW77077;

DT 16-NOV-1998 (first entry)

DE Human interleukin 18.

XX Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;

KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;

KW chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.

XX Homo sapiens.

XX EP861663-A2.

XX 02-SEP-1998.

PF 24-FEB-1998; 98EP-00301352.

XX 25-FEB-1997; 97JP-00055468.

XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.

XX Gillespie MT, Horwood NJ, Udagawa N, Kurimoto M;

DR N-PSDB; AAV48226.

XX Use of interleukin-18 to inhibit osteoclast formation - in treatment of

PT e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome, osteosarcoma,

PT chronic rheumatoid arthritis, deformity ostitis, primary hyperthyroidism

PT and osteoporosis.

XX Claim 4; Page 18; 56pp; English.

XX Interleukin-18 (IL-18) or a functional equivalent can be used for

CC inhibition of osteoclast formation. IL-18 is used for treating or

CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma

CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid

CC arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and

CC osteoporosis

XX Sequence 157 AA;

Query Match 53.5%; Score 84; DB 2; Length 157;

Best Local Similarity 100.0%; Pred. No. 1.9e-83;

Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKMQFESSSYEGYFLACEKERDL 133

Db 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKMQFESSSYEGYFLACEKERDL 133

QY 134 FKLILKKEDELGDRSIMFTVQNE 157

Db 134 FKLILKKEDELGDRSIMFTVQNE 157

Db 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKMQFESSSYEGYFLACEKERDL 133

QY 134 FKLILKKEDELGDRSIMFTVQNE 157

Db 134 FKLILKKEDELGDRSIMFTVQNE 157

## RESULT 22

AAW77083

ID AAW77083 standard; peptide; 157 AA.

XX

AC AAW77083;

DT 16-NOV-1998 (first entry)

XX Human interleukin 18 derivative 1.

XX Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;

KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;

KW chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.

XX Homo sapiens.

XX EP861663-A2.

XX 02-SEP-1998.

PF 24-FEB-1998; 98EP-00301352.

XX 25-FEB-1997; 97JP-00055468.

XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.

XX Gillespie MT, Horwood NJ, Udagawa N, Kurimoto M;

DR WPI; 1998-448964/39.

XX Use of interleukin-18 to inhibit osteoclast formation - in treatment of

PT e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome, osteosarcoma,

PT chronic rheumatoid arthritis, deformity ostitis, primary hyperthyroidism

PT and osteoporosis.

XX Disclosure; Page 30; 56pp; English.

XX Interleukin-18 (IL-18) or a functional equivalent can be used for

CC inhibition of osteoclast formation. IL-18 is used for treating or

CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma

CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid

CC arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and

CC osteoporosis

XX Sequence 157 AA;

Query Match 53.5%; Score 84; DB 2; Length 157;

Best Local Similarity 100.0%; Pred. No. 1.9e-83;

Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKMQFESSSYEGYFLACEKERDL 133

Db 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKMQFESSSYEGYFLACEKERDL 133

QY 134 FKLILKKEDELGDRSIMFTVQNE 157

Db 134 FKLILKKEDELGDRSIMFTVQNE 157

## RESULT 23

AAW48961

ID AAW48961 standard; peptide; 157 AA.

XX

AC AAW48961;

DT 25-SEP-1998 (first entry)

AC	AAW48962;	
XX		
XX	25-SEP-1998 (first entry)	
DE	Mutant human interferon-gamma inducing factor IGIF/MUT21.	
XX		
KW	Interferon-gamma inducing factor; interferon-gamma; killer cell;	
KW	antitumour agent; antiviral agent; antimicrobial agent; tumour; IGIF;	
KW	hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;	
KW	osteoporosis; thrombopenia; acquired immunodeficiency syndrome.	
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 38	
FT	/note= "changed from Cys in wild-type to Ser in mutant"	
XX		
XX	EP845530-A2.	
XX		
PD	03-JUN-1998.	
XX		
PF	28-NOV-1997; 97EP-00309632.	
XX		
PR	29-NOV-1996; 96JP-00333037.	
PR	21-JAN-1997; 97JP-00020906.	
PR	14-NOV-1997; 97JP-00329715.	
XX		
PA	(HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.	
XX		
PI	Yamamoto K, Okamoto I, Kurimoto M;	
XX		
DR	WPI; 1998-288747/26.	
DR	N-PSDB; AAV32626.	
PT	Mutants of interferon-gamma inducing polypeptide - useful as antitumour,	
PT	antiviral, antimicrobial or anti-immunopathic agents.	
XX		
PS	Claim 5; Page 41; 59pp; English.	
XX		
CC	The present sequence represents the mutant human interferon-gamma	
CC	inducing factor IGIF/MUT21. The wild-type human interferon-gamma factor	
CC	sequence is shown in AAW48959. The invention provides for mutant human	
CC	and mouse interferon-gamma inducing factors (IGIF) in which one or more	
CC	cysteine residues are replaced with different residues at or away from	
CC	the consensus sequences shown in AAW48956-W48958. The mutant IGIFs are	
CC	capable of stimulating immunocompetent cells for the production of	
CC	interferon-gamma and are claimed to be less toxic, more active and stable	
CC	than the corresponding wild type interferon-gamma inducing factor. The	
CC	mutant IGIFs are also claimed to enhance killer cell cytotoxicity and/or	
CC	induce killer cell formation, and may therefore be useful as antitumour	
CC	agents, antitumour immunotherapeutics, antiviral agents and antimicrobial	
CC	agents. The mutant IGIFs are also claimed to be useful for treating	
CC	hepatitis, acquired immunodeficiency syndrome (AIDS), malaria,	
CC	tuberculosis, solid malignant tumours (e.g. renal carcinoma), rheumatism,	
CC	osteoporosis and thrombopenia caused by radiation- and chemo-therapy	
XX		
SQ	Sequence 157 AA;	
	Query Match	53.5%; Score 84; DB 2; Length 157;
	Best Local Similarity	100.0%; Pred. No. 1.9e-83;
	Matches 84; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	74 LSCENKIISFKENNPDDNIKOTKSDLIFFORSVPGHDNKNMFFSSSYEGYFLACEKERDL	133
DB	74 LSCENKIISFKENNPDDNIKOTKSDLIFFORSVPGHDNKNMFFSSSYEGYFLACEKERDL	133
QY	134 FKLIKKKEDELGDRSIMFTVQNE	157
DB	134 FKLIKKKEDELGDRSIMFTVQNE	157

AAAY57570  
ID AAAY57570 standard; protein; 157 AA.  
XX  
AC AAAY57570;  
XX  
DT 06-MAR-2000 (first entry)  
XX  
DE Human interleukin 18 protein sequence SEQ ID NO:1.  
XX  
KW Human; interleukin 18; IL-18; potentiator; IGIF; tumour; cancer;  
KW interferon-gamma-inducing factor; growth inhibition; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO959565-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 20-MAY-1999; 99WO-US011160.  
XX  
PR 21-MAY-1998; 98US-0086560P.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
PI Johnson RK;  
XX  
DR WPI; 2000-062368/05.  
XX  
PT New polypeptides, useful for preparation of composition for preventing  
PT and/or treating cancer by inhibiting tumor growth.  
XX  
PS Claim 1; Page 49-50; 53pp; English.  
XX  
CC The present sequence represents human interleukin 18 (IL-18). The present  
CC invention describes a compound comprising human or murine IL-18 in  
CC combination with a chemotherapeutic agent (I). Also described are: (1) a  
CC method of preventing and/or treating cancer in a mammal comprising the  
CC administration of a cancer inhibiting amount of (I) comprising the IL-18  
CC protein and the chemotherapeutic agent and optionally a pharmaceutically  
CC acceptable carrier; and (2) a method of inhibiting the growth of tumour  
CC cells in a mammal sensitive to a composition comprising human IL-18  
CC and/or murine IL-18 and the chemotherapeutic agent (and optionally a  
CC pharmaceutically acceptable carrier), comprising administering to a  
CC mammal afflicted with the tumour cells an effective tumour cell growth  
CC inhibiting amount of (I). The IL-18 protein in conjunction with a  
CC chemotherapeutic agent is useful in a method for preventing and/or  
CC treating cancer in mammals by inhibiting the growth of tumours or  
CC cancerous cells in mammals  
XX  
SQ Sequence 157 AA;  
  
Query Match 53.5%; Score 84; DB 3; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.9e-83;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 74 LSCENKIIISFKENPPDNIDKTSDIIFQRSVPGHDKMKQFESSYEGYFLACEKERDL 133  
DB 74 LSCENKIIISFKENPPDNIDKTSDIIFQRSVPGHDKMKQFESSYEGYFLACEKERDL 133  
  
QY 134 FKLLKKEDELGDRSIMFTVQNEED 157  
DB 134 FKLLKKEDELGDRSIMFTVQNEED 157  
  
Search completed: January 30, 2006, 08:55:05  
Job time : 135 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2006, 08:58:16 ; Search time 116 Seconds  
(without alignments)  
565.510 Million cell updates/sec

Title: US-09-716-356A-6  
Perfect score: 157  
Sequence: 1 YFGKLESLVIRNLNDQVL.....LKXDELGRSIFMTVQNE 157

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Published Applications AA Main:  
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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length	ID Description
1	156	99.4	157 2 US-08-996-140-1 Sequence 1, Appli
2	156	99.4	157 3 US-09-752-510-6 Sequence 6, Appli
3	156	99.4	157 3 US-09-924-099-21 Sequence 21, Appli
4	156	99.4	157 4 US-10-327-089-1 Sequence 1, Appli
5	156	99.4	157 4 US-10-349-023-26 Sequence 26, Appli
6	156	99.4	157 5 US-10-730-034-1 Sequence 1, Appli
7	156	99.4	193 4 US-10-646-308-13 Sequence 13, Appli
8	84	53.5	157 3 US-09-775-046-9 Sequence 9, Appli
9	84	53.5	157 3 US-09-030-061-6 Sequence 6, Appli
10	84	53.5	157 3 US-09-030-061-20 Sequence 20, Appli
11	84	53.5	157 3 US-09-030-061-21 Sequence 21, Appli
12	84	53.5	157 4 US-10-100-057-6 Sequence 6, Appli
13	84	53.5	157 4 US-10-100-057-20 Sequence 20, Appli
14	84	53.5	157 4 US-10-100-057-21 Sequence 21, Appli
15	84	53.5	157 4 US-10-094-153-2 Sequence 2, Appli
16	84	53.5	157 4 US-10-094-153-6 Sequence 6, Appli
17	84	53.5	157 4 US-10-094-153-7 Sequence 7, Appli
18	84	53.5	157 4 US-10-094-153-8 Sequence 8, Appli
19	84	53.5	157 4 US-10-094-153-10 Sequence 10, Appli
20	84	53.5	157 4 US-10-260-576-4 Sequence 4, Appli
21	84	53.5	157 4 US-10-260-576-6 Sequence 6, Appli
22	84	53.5	157 4 US-10-260-576-7 Sequence 7, Appli
23	84	53.5	157 4 US-10-297-136-1 Sequence 1, Appli
24	84	53.5	157 4 US-10-311-491-3 Sequence 3, Appli
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26	84	53.5	157 4 US-10-397-786A-3 Sequence 3, Appli
27	84	53.5	157 4 US-10-280-576-1 Sequence 1, Appli

28	84	53.5	157 4 US-10-646-308-14 Sequence 14, Appli
29	84	53.5	157 5 US-10-872-198-98 Sequence 98, Appli
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31	84	53.5	157 5 US-10-823-964A-4 Sequence 4, Appli
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34	84	53.5	157 6 US-11-021-951-98 Sequence 98, Appli
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56	81	51.6	157 3 US-09-030-061-25 Sequence 25, Appli
57	81	51.6	157 4 US-10-100-057-25 Sequence 25, Appli
58	81	51.6	157 4 US-10-280-576-11 Sequence 11, Appli
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61	70	44.6	157 5 US-10-823-964A-7 Sequence 7, Appli
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66	53	33.8	157 3 US-09-030-061-23 Sequence 23, Appli
67	53	33.8	157 4 US-10-100-057-23 Sequence 23, Appli
68	53	33.8	157 4 US-10-260-576-9 Sequence 9, Appli
69	50	31.8	150 3 US-09-752-510-2 Sequence 2, Appli
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72	50	31.8	157 4 US-10-100-057-24 Sequence 24, Appli
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74	50	31.8	157 4 US-10-260-576-10 Sequence 10, Appli
75	50	31.8	157 4 US-10-260-576-12 Sequence 12, Appli
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82	14	8.9	14 3 US-10-823-964A-24 Sequence 24, Appli
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84	14	8.9	14 4 US-09-030-061-12 Sequence 12, Appli
85	13	8.3	13 3 US-10-100-057-12 Sequence 12, Appli
86	13	8.3	13 3 US-09-752-510-7 Sequence 7, Appli
87	13	8.3	13 3 US-09-030-061-11 Sequence 11, Appli
88	13	8.3	13 4 US-10-100-057-11 Sequence 11, Appli
89	13	8.3	154 3 US-09-917-265-5 Sequence 5, Appli
90	13	8.3	154 5 US-10-821-670-5 Sequence 5, Appli
91	13	8.3	157 5 US-09-917-265-12 Sequence 12, Appli
92	13	8.3	192 3 US-09-917-265-8 Sequence 8, Appli
93	13	8.3	192 5 US-09-917-265-8 Sequence 8, Appli
94	10	6.4	10 3 US-10-821-670-8 Sequence 8, Appli
95	10	6.4	10 3 US-09-752-510-1 Sequence 1, Appli
96	10	6.4	10 3 US-09-752-510-3 Sequence 3, Appli
97	10	6.4	10 3 US-09-030-061-10 Sequence 10, Appli
98	10	6.4	10 4 US-10-100-057-10 Sequence 10, Appli
99	10	6.4	10 4 US-10-100-057-15 Sequence 15, Appli
100	10	6.4	10 4 US-10-260-576-27 Sequence 27, Appli

## ALIGNMENTS

## RESULT 1

US-08-996-140-1  
; Sequence 1, Application US/08996140  
; Publication No. US20030190318A1  
; GENERAL INFORMATION:  
; APPLICANT: TORIGOE, Kakuji  
; APPLICANT: USHIO, Shimpel  
; APPLICANT: KUNIKATA, Toshio  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/996,140  
; FILING DATE: 22-DEC-1997  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: JP 356,426/1996  
; FILING DATE: 26-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 52,526/1997  
; FILING DATE: 21-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 163,490/1997  
; FILING DATE: 6-JUN-1997  
; APPLICATION DATA:  
; APPLICATION NUMBER: JP 215,490/1997  
; FILING DATE: 28-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: TORIGOE-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-996-140-1

Query Match 99.4%; Score 156; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.4e-147;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60  
DB 1 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSKENKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKNQFESSY 120  
DB 61 AVTISVKCEKISXLSKENKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKNQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

## RESULT 2

US-09-752-510-6  
; Sequence 6, Application US/09752510  
; Publication No. US20010018212A1  
; GENERAL INFORMATION:  
; APPLICANT: AKITA, Kenji  
; NUKADA, Yoshiyuki  
; FUJII, Mitsukiyo  
; TANIMOTO, Tadao  
; KURIMOTO, Masashi  
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street N.W., Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/752,510  
; FILING DATE: 03-Jan-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/721,018  
; FILING DATE: <unknown>  
; APPLICATION NUMBER: JP 96-067434  
; FILING DATE: 29-FEB-1996  
; APPLICATION NUMBER: JP not yet received  
; FILING DATE: 20-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: AKITA-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: "Xaa" in position 73 is either  
; 'ile' or 'Thr'  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-752-510-6

Query Match 99.4%; Score 156; DB 3; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.4e-147;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60  
DB 1 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSKENKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKNQFESSY 120  
DB 61 AVTISVKCEKISXLSKENKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKNQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

```
RESULT 3
US-09-924-099-21
; Sequence 21, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 21
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (73)
; OTHER INFORMATION: "Xaa" means an amino acid of isoleucine or threonine.
US-09-924-099-21

Query Match          99.4%; Score 156; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.4e-147;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60

Qy 61 AVTISVCKEKISXLSKCNKIISFKEMNPPDNKTKSDIIFQFQSVPGHNDKMQFESSY 120
Db 61 AVTISVCKEKISXLSKCNKIISFKEMNPPDNKTKSDIIFQFQSVPGHNDKMQFESSY 120

Qy 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNE 157

RESULT 4
US-10-327-069-1
; Sequence 1, Application US/10327069
; Publication No. US20030129184A1
; GENERAL INFORMATION:
; APPLICANT: KENKYUJO
; APPLICANT: KUNIKATA, Toshio
; APPLICANT: TANIGUCHI, Mutsuko
; APPLICANT: KOHNO, Keizo
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/349,023
; FILING DATE: 23-Jan-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/556,972
; FILING DATE: 24-Apr-2000
; APPLICATION NUMBER: US/08/996,338
; FILING DATE: 22-DEC-1997
```

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SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/327,069
FILING DATE: 24-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/558,818
FILING DATE: NO. US20030129184A1ember 15, 1995
APPLICATION NUMBER: JP 58,240/95
FILING DATE: February 23, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELICI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-327-069-1

Query Match          99.4%; Score 156; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.4e-147;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60

Qy 61 AVTISVCKEKISXLSKCNKIISFKEMNPPDNKTKSDIIFQFQSVPGHNDKMQFESSY 120
Db 61 AVTISVCKEKISXLSKCNKIISFKEMNPPDNKTKSDIIFQFQSVPGHNDKMQFESSY 120

Qy 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNE 157

RESULT 5
US-10-349-023-26
; Sequence 26, Application US/10349023
; Publication No. US20030133919A1
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: OKURA, Takanori
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/349,023
; FILING DATE: 23-Jan-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/556,972
; FILING DATE: 24-Apr-2000
; APPLICATION NUMBER: US/08/996,338
; FILING DATE: 22-DEC-1997
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APPLICATION NUMBER: JP 74,697/1997  
FILING DATE: 12-MAR-1997  
APPLICATION NUMBER: JP 215,488/1997  
FILING DATE: 28-JUL-1997  
APPLICATION NUMBER: JP 291,837/1997  
FILING DATE: 09-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: TORIGOE-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-10-349-023-26

Query Match 99.4%; Score 156; DB 4; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.4e-147;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKOTKSDIIFQSVPGHDNKKMFESSY 120  
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKOTKSDIIFQSVPGHDNKKMFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 6  
US-10-730-034-1  
Sequence 1, Application US/10730034  
Publication No. US20040253303A1  
GENERAL INFORMATION:  
APPLICANT: Takanori OKURA  
Kakuji TORIGOE  
Masashi KURIMOTO  
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE  
OF INDUCING THE PRODUCTION OF INTERFERON-  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10730,034  
FILING DATE: 09-Dec-2003  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/884,324  
FILING DATE: 27-JUN-1997  
APPLICATION NUMBER: JP 185,305/96  
FILING DATE: 27-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: OKURA-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-730-034-1

Query Match 99.4%; Score 156; DB 5; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.4e-147;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKOTKSDIIFQSVPGHDNKKMFESSY 120  
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKOTKSDIIFQSVPGHDNKKMFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 7  
US-10-646-308-13  
Sequence 13, Application US/10646308  
Publication No. US20040136992A1  
GENERAL INFORMATION:  
APPLICANT: BURTON, Paul B. J.  
APPLICANT: DEISHER, Theresa A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE  
FILE REFERENCE: 3432-B  
CURRENT APPLICATION NUMBER: US/10/646,308  
CURRENT FILING DATE: 2003-08-21  
PRIOR APPLICATION NUMBER: --to be assigned--  
PRIOR FILING DATE: 2003-08-12  
PRIOR APPLICATION NUMBER: 60/406,418  
PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 13  
LENGTH: 193  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (73)-(73)  
OTHER INFORMATION: The 'Xaa' at location 73 stands for Thr, or Ile.  
US-10-646-308-13

Query Match 99.4%; Score 156; DB 4; Length 193;  
Best Local Similarity 100.0%; Pred. No. 1.7e-147;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60  
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 96

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKOTKSDIIFQSVPGHDNKKMFESSY 120  
DB 97 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKOTKSDIIFQSVPGHDNKKMFESSY 156

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

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RESULT 8
US-09-775-046-9
; Sequence 9, Application US/09775046
; Patent No. US20020102234A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Debets, Johannes Eduard Maria Antonius
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01073K
; CURRENT APPLICATION NUMBER: US/09/775,046
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/179,638
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 9
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-046-9

Query Match          53.5%; Score 84; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNIKDKTSIIFFORSVPGHDKMKQFESSSYEGYFLACEKERDL 133
DB 74 LSCENKIISFKEMNPPDNIKDKTSIIFFORSVPGHDKMKQFESSSYEGYFLACEKERDL 133

QY 134 FKLILKKEDELGDRSIMFTVQNE 157
DB 134 FKLILKKEDELGDRSIMFTVQNE 157

RESULT 9
US-09-030-061-6
; Sequence 6, Application US/09030061
; Publication No. US20030095946A1
; GENERAL INFORMATION:
; APPLICANT: GILLISPIE, Matthew Todd
; APPLICANT: HORWOOD, Nicole Joy
; APPLICANT: UDAGAWA, No. US20030095946Aluyuki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,061
; FILING DATE: 25-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 55,468/1997
; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197

QY 74 LSCENKIISFKEMNPPDNIKDKTSIIFFORSVPGHDKMKQFESSSYEGYFLACEKERDL 133
DB 74 LSCENKIISFKEMNPPDNIKDKTSIIFFORSVPGHDKMKQFESSSYEGYFLACEKERDL 133

QY 134 FKLILKKEDELGDRSIMFTVQNE 157
DB 134 FKLILKKEDELGDRSIMFTVQNE 157

RESULT 10
US-09-030-061-20
; Sequence 20, Application US/09030061
; Publication No. US20030095946A1
; GENERAL INFORMATION:
; APPLICANT: GILLISPIE, Matthew Todd
; APPLICANT: HORWOOD, Nicole Joy
; APPLICANT: UDAGAWA, No. US20030095946Aluyuki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,061
; FILING DATE: 25-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 55,468/1997
; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197

QY 74 LSCENKIISFKEMNPPDNIKDKTSIIFFORSVPGHDKMKQFESSSYEGYFLACEKERDL 133
DB 74 LSCENKIISFKEMNPPDNIKDKTSIIFFORSVPGHDKMKQFESSSYEGYFLACEKERDL 133

QY 134 FKLILKKEDELGDRSIMFTVQNE 157
DB 134 FKLILKKEDELGDRSIMFTVQNE 157
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TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-030-061-6

Query Match          53.5%; Score 84; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNIKDKTSIIFFORSVPGHDKMKQFESSSYEGYFLACEKERDL 133
DB 74 LSCENKIISFKEMNPPDNIKDKTSIIFFORSVPGHDKMKQFESSSYEGYFLACEKERDL 133

QY 134 FKLILKKEDELGDRSIMFTVQNE 157
DB 134 FKLILKKEDELGDRSIMFTVQNE 157

RESULT 10
US-09-030-061-20
; Sequence 20, Application US/09030061
; Publication No. US20030095946A1
; GENERAL INFORMATION:
; APPLICANT: GILLISPIE, Matthew Todd
; APPLICANT: HORWOOD, Nicole Joy
; APPLICANT: UDAGAWA, No. US20030095946Aluyuki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,061
; FILING DATE: 25-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 55,468/1997
; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197

QY 74 LSCENKIISFKEMNPPDNIKDKTSIIFFORSVPGHDKMKQFESSSYEGYFLACEKERDL 133
DB 74 LSCENKIISFKEMNPPDNIKDKTSIIFFORSVPGHDKMKQFESSSYEGYFLACEKERDL 133

QY 134 FKLILKKEDELGDRSIMFTVQNE 157
DB 134 FKLILKKEDELGDRSIMFTVQNE 157
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```
Query Match          53.5%; Score 84; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNIKDKTSIIFFORSVPGHDKMKQFESSSYEGYFLACEKERDL 133
DB 74 LSCENKIISFKEMNPPDNIKDKTSIIFFORSVPGHDKMKQFESSSYEGYFLACEKERDL 133

QY 134 FKLILKKEDELGDRSIMFTVQNE 157
DB 134 FKLILKKEDELGDRSIMFTVQNE 157
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QY 134 FKILKKEDELGDRSIMFTVQNE 157  
Db 134 FKILKKEDELGDRSIMFTVQNE 157

## RESULT 11

US-09-030-061-21  
; Sequence 21, Application US/09030061  
; Publication No. US20030095946A1  
; GENERAL INFORMATION:  
; APPLICANT: GILLISPIE, Matthew Todd  
; APPLICANT: HORWOOD, Nicole Joy  
; APPLICANT: UDAGAWA, No. US20030095946A1uyuki  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,061  
; FILING DATE: 25-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 55,468/1997  
; FILING DATE: 25-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: GILLISPIE-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-030-061-21

Query Match 53.5%; Score 84; DB 3; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.3e-75;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 74 LSCENKIISFKEMNPPDNKDTSDIIFQSVPGHDKMQFESSSYEGYFLACEKERDL 133  
Db 74 LSCENKIISFKEMNPPDNKDTSDIIFQSVPGHDKMQFESSSYEGYFLACEKERDL 133  
QY 134 FKILKKEDELGDRSIMFTVQNE 157  
Db 134 FKILKKEDELGDRSIMFTVQNE 157

## RESULT 12

US-10-100-057-6  
; Sequence 6, Application US/10100057  
; Publication No. US20020150555A1  
; GENERAL INFORMATION:  
; APPLICANT: GILLISPIE, Matthew Todd  
; APPLICANT: HORWOOD, Nicole Joy  
; APPLICANT: UDAGAWA, No. US20020150555A1uyuki  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT

NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/100,057  
FILING DATE: 19-Mar-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/030,061  
FILING DATE: 25-FEB-1998  
APPLICATION NUMBER: JP 55,468/1997  
FILING DATE: 25-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: GILLISPIE-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-100-057-6  
Query Match 53.5%; Score 84; DB 4; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.3e-75;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 74 LSCENKIISFKEMNPPDNKDTSDIIFQSVPGHDKMQFESSSYEGYFLACEKERDL 133  
Db 74 LSCENKIISFKEMNPPDNKDTSDIIFQSVPGHDKMQFESSSYEGYFLACEKERDL 133  
QY 134 FKILKKEDELGDRSIMFTVQNE 157  
Db 134 FKILKKEDELGDRSIMFTVQNE 157  
RESULT 13  
US-10-100-057-20  
; Sequence 20, Application US/10100057  
; Publication No. US20020150555A1  
; GENERAL INFORMATION:  
; APPLICANT: GILLISPIE, Matthew Todd  
; APPLICANT: HORWOOD, Nicole Joy  
; APPLICANT: UDAGAWA, No. US20020150555A1uyuki  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30

;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/100,057  
;; FILING DATE: 19-Mar-2002  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/030,061  
;; FILING DATE: 25-FEB-1998  
;; APPLICATION NUMBER: JP 55,468/1997  
;; FILING DATE: 25-FEB-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BROWDY, Roger L.  
;; REGISTRATION NUMBER: 25,618  
;; REFERENCE/DOCKET NUMBER: GILLISPIE=1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 737-3528  
;; TELEFAX: (202) 737-3528  
;; INFORMATION FOR SEQ ID NO: 20:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 157 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-10-100-057-20  
  
Query Match 53.5%; Score 84; DB 4; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.3e-75;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 74 LSCENKIISFKEMNPPDNIKDKSDIIFQSVPGHDKMKQFESSYEGYFLACEKERDL 133  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
74 LSCENKIISFKEMNPPDNIKDKSDIIFQSVPGHDKMKQFESSYEGYFLACEKERDL 133  
  
Qy 134 FKILKKEDELGDRSIMFTVQNE 157  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
134 FKILKKEDELGDRSIMFTVQNE 157  
  
RESULT 14  
US-10-100-057-21  
; Sequence 21, Application US/10100057  
; Publication No. US20020150555A1  
; GENERAL INFORMATION:  
; APPLICANT: GILLISPIE, Matthew Todd  
; HORWOOD, Nicole Joy  
; UDAGAWA, No. US20020150555A1  
; KURIMOTO, Masashi  
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/100,057  
; FILING DATE: 19-Mar-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,061  
; FILING DATE: 25-FEB-1998  
; APPLICATION NUMBER: JP 55,468/1997  
; FILING DATE: 25-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: GILLISPIE=1  
; TELECOMMUNICATION INFORMATION:

;;  
;; TELEPHONE: (202) 628-5197  
;; TELEFAX: (202) 737-3528  
;; INFORMATION FOR SEQ ID NO: 21:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 157 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 21:  
US-10-100-057-21  
  
Query Match 53.5%; Score 84; DB 4; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.3e-75;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 74 LSCENKIISFKEMNPPDNIKDKSDIIFQSVPGHDKMKQFESSYEGYFLACEKERDL 133  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
74 LSCENKIISFKEMNPPDNIKDKSDIIFQSVPGHDKMKQFESSYEGYFLACEKERDL 133  
  
Qy 134 FKILKKEDELGDRSIMFTVQNE 157  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
134 FKILKKEDELGDRSIMFTVQNE 157  
  
RESULT 15  
US-10-094-153-2  
; Sequence 2, Application US/10094153  
; Publication No. US20020169291A1  
; GENERAL INFORMATION:  
; APPLICANT: Dinarello, Charles  
; APPLICANT: Kim, Soo Hyun  
; TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use  
; FILE REFERENCE: 475  
; CURRENT APPLICATION NUMBER: US/10/094,153  
; PRIOR FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: 60/274,327  
; PRIOR FILING DATE: 2001-03-08  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 2  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-094-153-2  
  
Query Match 53.5%; Score 84; DB 4; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.3e-75;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 74 LSCENKIISFKEMNPPDNIKDKSDIIFQSVPGHDKMKQFESSYEGYFLACEKERDL 133  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
74 LSCENKIISFKEMNPPDNIKDKSDIIFQSVPGHDKMKQFESSYEGYFLACEKERDL 133  
  
Qy 134 FKILKKEDELGDRSIMFTVQNE 157  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
134 FKILKKEDELGDRSIMFTVQNE 157  
  
RESULT 16  
US-10-094-153-6  
; Sequence 6, Application US/10094153  
; Publication No. US20020169291A1  
; GENERAL INFORMATION:  
; APPLICANT: Dinarello, Charles  
; APPLICANT: Kim, Soo Hyun  
; TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use  
; FILE REFERENCE: 475  
; CURRENT APPLICATION NUMBER: US/10/094,153  
; PRIOR FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: 60/274,327  
; PRIOR FILING DATE: 2001-03-08  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: Patent in version 3.1

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; SEQ ID NO 6
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-6

Query Match          53.5%; Score 84; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133
    |||||||
Db 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133
    |||||||

QY 134 FKILKKEDELGDRSIMFTVQNEED 157
    |||||||
Db 134 FKILKKEDELGDRSIMFTVQNEED 157
    |||||||

RESULT 17
US-10-094-153-7
; Sequence 7, Application US/10094153
; Publication No. US20020169291A1
; GENERAL INFORMATION:
; APPLICANT: Dinarello, Charles
; TITLE OF INVENTION: Interleukin-18 Mutants, Their Production and use
; FILE REFERENCE: 475
; CURRENT APPLICATION NUMBER: US/10/094,153
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/274,327
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-7

Query Match          53.5%; Score 84; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133
    |||||||
Db 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133
    |||||||

QY 134 FKILKKEDELGDRSIMFTVQNEED 157
    |||||||
Db 134 FKILKKEDELGDRSIMFTVQNEED 157
    |||||||

RESULT 18
US-10-094-153-8
; Sequence 8, Application US/10094153
; Publication No. US20020169291A1
; GENERAL INFORMATION:
; APPLICANT: Dinarello, Charles
; TITLE OF INVENTION: Interleukin-18 Mutants, Their Production and use
; FILE REFERENCE: 475
; CURRENT APPLICATION NUMBER: US/10/094,153
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/274,327
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-8

Query Match          53.5%; Score 84; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133
    |||||||
Db 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133
    |||||||

QY 134 FKILKKEDELGDRSIMFTVQNEED 157
    |||||||
Db 134 FKILKKEDELGDRSIMFTVQNEED 157
    |||||||

RESULT 19
US-10-094-153-10
; Sequence 10, Application US/10094153
; Publication No. US20020169291A1
; GENERAL INFORMATION:
; APPLICANT: Dinarello, Charles
; TITLE OF INVENTION: Interleukin-18 Mutants, Their Production and use
; FILE REFERENCE: 475
; CURRENT APPLICATION NUMBER: US/10/094,153
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/274,327
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-10

Query Match          53.5%; Score 84; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133
    |||||||
Db 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133
    |||||||

QY 134 FKILKKEDELGDRSIMFTVQNEED 157
    |||||||
Db 134 FKILKKEDELGDRSIMFTVQNEED 157
    |||||||

RESULT 20
US-10-260-576-4
; Sequence 4, Application US/10260576
; Publication No. US20030092130A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Koza
; APPLICANT: OKAMOTO, Iwao
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 7th Street N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/260,576
  FILING DATE: 01-Oct-2002
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/982,285
  FILING DATE: <Unknown>
  APPLICATION NUMBER: JP 333,037/96
  FILING DATE: No. US20030092130A1ember 29, 1996
  APPLICATION NUMBER: JP 20,906/97
  FILING DATE: January 21, 1997
  APPLICATION NUMBER: JP 10,053,503
  FILING DATE: No. US20030092130A1ember 14, 1997
ATTORNEY/AGENT INFORMATION:
  NAME: BROWDY, Roger L.
  REGISTRATION NUMBER: 25,618
  REFERENCE/DOCKET NUMBER: YAMAMOTO=15
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 202-628-5197
  TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 4:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 157 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-260-576-4

Query Match      53.5%; Score 84; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 LSCENKIISFKEMNPPDNKDKSDIIFFORSVPGHDKMOPFESSSYEGYFLACEKRD 133
Db 74 LSCENKIISFKEMNPPDNKDKSDIIFFORSVPGHDKMOPFESSSYEGYFLACEKRD 133

Qy 134 FKLILKKEDELGDRSIMFTVQNE 157
Db 134 FKLILKKEDELGDRSIMFTVQNE 157

RESULT 21
US-10-260-576-6
Sequence 6, Application US/10260576
Publication No. US20030092130A1
GENERAL INFORMATION:
  APPLICANT: YAMAMOTO, Kozo
  OKAMOTO, Iwao
  KURIMOTO, Masashi
  TITLE OF INVENTION: POLYPEPTIDES
  NUMBER OF SEQUENCES: 51
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
    STREET: 419 7th Street N.W., Suite 300
    CITY: Washington
    STATE: D.C.
    COUNTRY: USA
    ZIP: 20004
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patent in Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/10/260,576
      FILING DATE: 01-Oct-2002
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/08/982,285
      FILING DATE: <Unknown>
      APPLICATION NUMBER: JP 333,037/96
      FILING DATE: No. US20030092130A1ember 29, 1996
      APPLICATION NUMBER: JP 20,906/97
      FILING DATE: January 21, 1997
      APPLICATION NUMBER: JP 10,053,503
      FILING DATE: No. US20030092130A1ember 14, 1997
    ATTORNEY/AGENT INFORMATION:
      NAME: BROWDY, Roger L.
      REGISTRATION NUMBER: 25,618
      APPLICATION NUMBER: US/08/982,285
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/260,576
  FILING DATE: 01-Oct-2002
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/982,285
  FILING DATE: <Unknown>
  APPLICATION NUMBER: JP 333,037/96
  FILING DATE: No. US20030092130A1ember 29, 1996
  APPLICATION NUMBER: JP 20,906/97
  FILING DATE: January 21, 1997
  APPLICATION NUMBER: JP 10,053,503
  FILING DATE: No. US20030092130A1ember 14, 1997
ATTORNEY/AGENT INFORMATION:
  NAME: BROWDY, Roger L.
  REGISTRATION NUMBER: 25,618
  REFERENCE/DOCKET NUMBER: YAMAMOTO=15
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 202-628-5197
  TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 157 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-260-576-6

Query Match      53.5%; Score 84; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 LSCENKIISFKEMNPPDNKDKSDIIFFORSVPGHDKMOPFESSSYEGYFLACEKRD 133
Db 74 LSCENKIISFKEMNPPDNKDKSDIIFFORSVPGHDKMOPFESSSYEGYFLACEKRD 133

Qy 134 FKLILKKEDELGDRSIMFTVQNE 157
Db 134 FKLILKKEDELGDRSIMFTVQNE 157

RESULT 22
US-10-260-576-7
Sequence 7, Application US/10260576
Publication No. US20030092130A1
GENERAL INFORMATION:
  APPLICANT: YAMAMOTO, Kozo
  OKAMOTO, Iwao
  KURIMOTO, Masashi
  TITLE OF INVENTION: POLYPEPTIDES
  NUMBER OF SEQUENCES: 51
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
    STREET: 419 7th Street N.W., Suite 300
    CITY: Washington
    STATE: D.C.
    COUNTRY: USA
    ZIP: 20004
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patent in Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/10/260,576
      FILING DATE: 01-Oct-2002
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/08/982,285
      FILING DATE: <Unknown>
      APPLICATION NUMBER: JP 333,037/96
      FILING DATE: No. US20030092130A1ember 29, 1996
      APPLICATION NUMBER: JP 20,906/97
      FILING DATE: January 21, 1997
      APPLICATION NUMBER: JP 10,053,503
      FILING DATE: No. US20030092130A1ember 14, 1997
    ATTORNEY/AGENT INFORMATION:
      NAME: BROWDY, Roger L.
      REGISTRATION NUMBER: 25,618
```

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; REFERENCE/DOCKET NUMBER: YAMAMOTO=15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-260-576-7

Query Match          53.5%; Score 84; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMQFESSSYEGYFLACEKERDL 133
Db 74 LSCENKIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMQFESSSYEGYFLACEKERDL 133

QY 134 FKILKKEDELGDRSIMFTVQNEED 157
Db 134 FKILKKEDELGDRSIMFTVQNEED 157

RESULT 23
US-10-297-136-1
; Sequence 1, Application US/10297136
; Publication No. US2003013292A1
; GENERAL INFORMATION:
; APPLICANT: ESSER, KLAUS M.
; APPLICANT: ROSENBERG, MARTIN
; APPLICANT: TAL-SINGER, RUTH
; APPLICANT: WOODNUTT, GARY
; APPLICANT: CHISARI, FRANCIS V.
; APPLICANT: DILLON, SUSAN B.
; TITLE OF INVENTION: Methods of Treating Viral Diseases with
; FILE OF INVENTION: IL-18 and IL-18 Combinations
; FILE REFERENCE: P51144
; CURRENT APPLICATION NUMBER: US/10/297,136
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/US01/17924
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/208,869
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-297-136-1

Query Match          53.5%; Score 84; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMQFESSSYEGYFLACEKERDL 133
Db 74 LSCENKIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMQFESSSYEGYFLACEKERDL 133

QY 134 FKILKKEDELGDRSIMFTVQNEED 157
Db 134 FKILKKEDELGDRSIMFTVQNEED 157

RESULT 24
US-10-311-491-3
; Sequence 3, Application US/10311491
; Publication No. US20030143198A1
; GENERAL INFORMATION:
; APPLICANT: Johanson, Kyung O.
```

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; APPLICANT: Kirkpatrick, Robert B.
; APPLICANT: Shatzman, Allan R.
; APPLICANT: Ho, Yen Sen
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: Method for Preparing a Physiologically
; TITLE OF INVENTION: Active IL-18 Polypeptide
; FILE REFERENCE: P51137
; CURRENT APPLICATION NUMBER: US/10/311,491
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/18804
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/211,832
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/224,128
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/264,923
; PRIOR FILING DATE: 2001-01-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-311-491-3

Query Match          53.5%; Score 84; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMQFESSSYEGYFLACEKERDL 133
Db 74 LSCENKIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMQFESSSYEGYFLACEKERDL 133

QY 134 FKILKKEDELGDRSIMFTVQNEED 157
Db 134 FKILKKEDELGDRSIMFTVQNEED 157

RESULT 25
US-10-105-080-10
; Sequence 10, Application US/10105080
; Publication No. US20030143203A1
; GENERAL INFORMATION:
; APPLICANT: SAMYANG GENEX CORPORATION
; TITLE OF INVENTION: RECOMBINANT ADENOVIRUSES EXPRESSING INTERLEUKIN-18 PROTEIN AND
; FILE OF INVENTION: GENE THERAPY USING THEM
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/105,080
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: KR 10-2001-78296
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 10
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Human mature inerleukin-18 mutant
US-10-105-080-10

Query Match          53.5%; Score 84; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMQFESSSYEGYFLACEKERDL 133
Db 74 LSCENKIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMQFESSSYEGYFLACEKERDL 133

QY 134 FKILKKEDELGDRSIMFTVQNEED 157
Db 134 FKILKKEDELGDRSIMFTVQNEED 157

Search completed: January 30, 2006, 09:09:50
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Job time : 117 secs

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